

SEQUENCE LISTING

<110> Jensen, Wayne A.
Lappin, Michael R.
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Andrews, Janet S.

<120> USE OF RECOMBINANT ANTIGENS TO DETERMINE THE IMMUNE
STATUS OF AN ANIMAL

<130> DI-9-1

<140> not yet assigned

<141> 2003-09-22

<140> 09/521,738

<141> 2000-03-09

<160> 36

<170> PatentIn Ver. 2.1

<210> 1

<211> 2013

<212> DNA

<213> Feline calicivirus

<220>

<221> CDS

<222> (1)..(2013)

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His Phe Lys Leu Val Ile Asn Pro Asn Asn Phe Leu Ser Val Gly Phe	
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Cys Ser Asn Pro Leu Met Cys Cys Tyr Pro Glu Leu Leu Pro Glu Phe	
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Gly Thr Val Trp Asp Cys Asp Arg Ser Pro Leu Glu Ile Tyr Leu Glu	
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Ser Ile Leu Gly Asp Asp Glu Trp Ala Ser Thr Phe Asp Ala Val Asp	
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Pro Val Val Pro Pro Met His Trp Gly Ala Ala Gly Lys Ile Phe Gln	
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Glu	Pro	Ser	Ala	Gln	Met	Ser	Thr	Ala	Ala	Asp	Met	Ala	Thr	Gly	Lys		
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 Gly Tyr Val Ile Arg Ser Ile Asp Val Phe Asn Ser Gln Ile Leu His
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act tcc aga cag tta tcg cta aat cat tac cta ctc cca cct gat tct 1824
 Thr Ser Arg Gln Leu Ser Leu Asn His Tyr Leu Leu Pro Pro Asp Ser
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 <213> Feline calicivirus

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 Gly Thr Val Trp Asp Cys Asp Arg Ser Pro Leu Glu Ile Tyr Leu Glu
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 Ser Ile Leu Gly Asp Asp Glu Trp Ala Ser Thr Phe Asp Ala Val Asp
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 Pro Val Val Pro Pro Met His Trp Gly Ala Ala Gly Lys Ile Phe Gln
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 Pro His Pro Gly Val Leu Met His His Leu Ile Gly Lys Val Ala Ala
 100 105 110

Gly Trp Asp Pro Asp Leu Pro Leu Ile Arg Leu Glu Ala Asp Asp Gly
 115 120 125
 Ser Ile Thr Ala Pro Glu Gln Gly Thr Met Val Gly Gly Val Ile Ala
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 Glu Pro Ser Ala Gln Met Ser Thr Ala Ala Asp Met Ala Thr Gly Lys
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 Ser Val Asp Ser Glu Trp Glu Ala Phe Phe Ser Phe His Thr Ser Val
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 Asn Trp Ser Thr Ser Glu Thr Gln Gly Lys Ile Leu Phe Lys Gln Ser
 180 185 190
 Leu Gly Pro Leu Leu Asn Pro Tyr Leu Glu His Leu Ala Lys Leu Tyr
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 Val Ala Trp Ser Gly Ser Ile Glu Val Arg Phe Ser Ile Ser Gly Ser
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 Gly Val Phe Gly Gly Lys Leu Ala Ala Ile Val Val Pro Pro Gly Val
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 Asp Pro Val Gln Ser Thr Ser Met Leu Gln Tyr Pro His Val Leu Phe
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 Asp Ala Arg Gln Val Glu Pro Val Ile Phe Cys Leu Pro Asp Leu Arg
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 Ser Thr Leu Tyr His Leu Met Ser Asp Thr Asp Thr Thr Ser Leu Val
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 Ile Met Val Tyr Asn Asp Leu Ile Asn Pro Tyr Ala Asn Asp Ala Asn
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 Ser Ser Gly Cys Ile Val Thr Val Glu Thr Lys Pro Gly Pro Asp Phe
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 Lys Phe His Leu Leu Lys Pro Pro Gly Ser Met Leu Thr His Gly Ser
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 Arg Tyr Trp Ser Asp Ile Thr Asp Phe Val Ile Arg Pro Phe Val Phe
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 Gln Ala Asn Arg His Phe Asp Phe Asn Gln Glu Thr Ala Gly Trp Ser
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 Thr Pro Arg Phe Arg Pro Ile Ser Val Thr Ile Thr Glu Gln Asn Gly
 385 390 395 400
 Ala Lys Leu Gly Ile Gly Val Ala Thr Asp Tyr Ile Val Pro Gly Ile
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Pro Asp Gly Trp Pro Asp Thr Thr Ile Pro Gly Glu Leu Ile Pro Ala
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 Gly Asp Tyr Ala Ile Thr Asn Gly Thr Gly Asn Asp Ile Thr Thr Ala
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 Gly Met Tyr Ile Cys Gly Ser Leu Gln Arg Ala Trp Gly Asp Lys Lys
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 Val Phe Gln Asp Asn His Val Gly Lys Lys Ala Gln Thr Ser Asp Asp
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 Thr Leu Ala Leu Leu Gly Tyr Thr Gly Ile Gly Glu Gln Ala Ile Gly
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 Ser Asp Arg Asp Arg Val Val Arg Ile Ser Thr Leu Pro Glu Thr Gly
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 Ala Arg Gly Gly Asn His Pro Ile Phe Tyr Lys Asn Ser Ile Lys Leu
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 Gly Tyr Val Ile Arg Ser Ile Asp Val Phe Asn Ser Gln Ile Leu His
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 Thr Ser Arg Gln Leu Ser Leu Asn His Tyr Leu Leu Pro Pro Asp Ser
 595 600 605
 Phe Ala Val Tyr Arg Ile Ile Asp Ser Asn Gly Ser Trp Phe Asp Ile
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 Gly Ile Asp Ser Asp Gly Phe Ser Phe Val Gly Val Ser Gly Phe Gly
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ggc gtc atc gct gaa ccc agc gcc cag atg tca aca gct gct gat atg	96
Gly Val Ile Ala Glu Pro Ser Ala Gln Met Ser Thr Ala Ala Asp Met	
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gcc acc ggg aaa agc gtt gat tct gag tgg gag gca ttc ttc tcc ttt	144
Ala Thr Gly Lys Ser Val Asp Ser Glu Trp Glu Ala Phe Phe Ser Phe	
35 40 45	
cac acc agc gtc aat tgg agt aca tct gaa acc caa gga aag att ctc	192
His Thr Ser Val Asn Trp Ser Thr Ser Glu Thr Gln Gly Lys Ile Leu	
50 55 60	
ttc aaa caa tcc tta ggc cct ttg ctc aac cca tat cta gaa cac ctt	240
Phe Lys Gln Ser Leu Gly Pro Leu Leu Asn Pro Tyr Leu Glu His Leu	
65 70 75 80	
gct aag cta tat gtt gcg tgg tct ggg tcg att gag gtt agg ttc tct	288
Ala Lys Leu Tyr Val Ala Trp Ser Gly Ser Ile Glu Val Arg Phe Ser	
85 90 95	
atc tct ggc tct ggt gtc ttt ggt ggg aag ctc gca gct att gtt gta	336
Ile Ser Gly Ser Gly Val Phe Gly Gly Lys Leu Ala Ala Ile Val Val	
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cct cct ggg gtt gat cca gtg cag agt act tcg atg cta caa tac ccc	384
Pro Pro Gly Val Asp Pro Val Gln Ser Thr Ser Met Leu Gln Tyr Pro	
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cat gtt ttg ttt gat gct cgt cag gtg gaa cca gtt atc ttc tgt ctt	432
His Val Leu Phe Asp Ala Arg Gln Val Glu Pro Val Ile Phe Cys Leu	
130 135 140	
cct gat cta aga agc acc ctg tac cac ctt atg tct gac act gac act	480
Pro Asp Leu Arg Ser Thr Leu Tyr His Leu Met Ser Asp Thr Asp Thr	
145 150 155 160	
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Thr Ser Leu Val Ile Met Val Tyr Asn Asp Leu Ile Asn Pro Tyr Ala	
165 170 175	
aat gat gcc aac tct tct ggg tgt att gtc act gtc gag aca aaa cct	576
Asn Asp Ala Asn Ser Ser Gly Cys Ile Val Thr Val Glu Thr Lys Pro	
180 185 190	
ggc cct gac ttc aag ttt cac ctc ctt aag cca ccc gga tct atg cta	624
Gly Pro Asp Phe Lys Phe His Leu Leu Lys Pro Pro Gly Ser Met Leu	
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Thr His Gly Ser Ile Pro Ser Asp Leu Ile Pro Lys Thr Ser Ser Leu	

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Ala Gly Trp Ser Thr Pro Arg Phe Arg Pro Ile Ser Val Thr Ile Thr			
	260	265	270
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Glu Gln Asn Gly Ala Lys Leu Gly Ile Gly Val Ala Thr Asp Tyr Ile			
	275	280	285
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Val Pro Gly Ile Pro Asp Gly Trp Pro Asp Thr Thr Ile Pro Gly Glu			
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Leu Ile Pro Ala Gly Asp Tyr Ala Ile Thr Asn Gly Thr Gly Asn Asp			
	305	310	315
atc acc acg gct aca gga tat gac act gct gat ata att aag aac aat			1008
Ile Thr Thr Ala Thr Gly Tyr Asp Thr Ala Asp Ile Ile Lys Asn Asn			
	325	330	335
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Thr Asn Phe Arg Gly Met Tyr Ile Cys Gly Ser Leu Gln Arg Ala Trp			
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ggt gat aag aaa att tcc aac act gcc ttt atc acc act gcc acc cta			1104
Gly Asp Lys Lys Ile Ser Asn Thr Ala Phe Ile Thr Thr Ala Thr Leu			
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Ser Lys Ile Val Val Phe Gln Asp Asn His Val Gly Lys Lys Ala Gln			
	385	390	395
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Thr Ser Asp Asp Thr Leu Ala Leu Leu Gly Tyr Thr Gly Ile Gly Glu			
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Gln Ala Ile Gly Ser Asp Arg Asp Arg Val Val Arg Ile Ser Thr Leu			
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cct gaa act ggt gct cga ggc ggt aac cac cca att ttc tac aag aac			1344
Pro Glu Thr Gly Ala Arg Gly Gly Asn His Pro Ile Phe Tyr Lys Asn			
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caa atc ttg cac act tcc aga cag tta tcg cta aat cat tac cta ctc 1440
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 Trp Phe Asp Ile Gly Ile Asp Ser Asp Gly Phe Ser Phe Val Gly Val
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 Ser Gly Phe Gly Lys Leu Glu Phe Pro Leu Ser Ala Ser Tyr Met Gly
 515 520 525

ata caa ttg gca aag atc cgg ctt gcc tct aac att agg agt ccc atg 1632
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 Thr Lys Leu
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<210> 4
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 <213> Feline calicivirus

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 Ala Thr Gly Lys Ser Val Asp Ser Glu Trp Glu Ala Phe Phe Ser Phe
 35 40 45
 His Thr Ser Val Asn Trp Ser Thr Ser Glu Thr Gln Gly Lys Ile Leu
 50 55 60
 Phe Lys Gln Ser Leu Gly Pro Leu Leu Asn Pro Tyr Leu Glu His Leu
 65 70 75 80
 Ala Lys Leu Tyr Val Ala Trp Ser Gly Ser Ile Glu Val Arg Phe Ser
 85 90 95
 Ile Ser Gly Ser Gly Val Phe Gly Gly Lys Leu Ala Ala Ile Val Val
 100 105 110

Pro Pro Gly Val Asp Pro Val Gln Ser Thr Ser Met Leu Gln Tyr Pro
 115 120 125
 His Val Leu Phe Asp Ala Arg Gln Val Glu Pro Val Ile Phe Cys Leu
 130 135 140
 Pro Asp Leu Arg Ser Thr Leu Tyr His Leu Met Ser Asp Thr Asp Thr
 145 150 155 160
 Thr Ser Leu Val Ile Met Val Tyr Asn Asp Leu Ile Asn Pro Tyr Ala
 165 170 175
 Asn Asp Ala Asn Ser Ser Gly Cys Ile Val Thr Val Glu Thr Lys Pro
 180 185 190
 Gly Pro Asp Phe Lys Phe His Leu Leu Lys Pro Pro Gly Ser Met Leu
 195 200 205
 Thr His Gly Ser Ile Pro Ser Asp Leu Ile Pro Lys Thr Ser Ser Leu
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 Trp Ile Gly Asn Arg Tyr Trp Ser Asp Ile Thr Asp Phe Val Ile Arg
 225 230 235 240
 Pro Phe Val Phe Gln Ala Asn Arg His Phe Asp Phe Asn Gln Glu Thr
 245 250 255
 Ala Gly Trp Ser Thr Pro Arg Phe Arg Pro Ile Ser Val Thr Ile Thr
 260 265 270
 Glu Gln Asn Gly Ala Lys Leu Gly Ile Gly Val Ala Thr Asp Tyr Ile
 275 280 285
 Val Pro Gly Ile Pro Asp Gly Trp Pro Asp Thr Thr Ile Pro Gly Glu
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 Leu Ile Pro Ala Gly Asp Tyr Ala Ile Thr Asn Gly Thr Gly Asn Asp
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 Gly Asp Lys Lys Ile Ser Asn Thr Ala Phe Ile Thr Thr Ala Thr Leu
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 Asp Gly Asp Asn Asn Asn Lys Ile Asn Pro Cys Asn Thr Ile Asp Gln
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 Ser Lys Ile Val Val Phe Gln Asp Asn His Val Gly Lys Lys Ala Gln
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 Thr Ser Asp Asp Thr Leu Ala Leu Leu Gly Tyr Thr Gly Ile Gly Glu
 405 410 415

Gln Ala Ile Gly Ser Asp Arg Asp Arg Val Val Arg Ile Ser Thr Leu
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 Pro Glu Thr Gly Ala Arg Gly Gly Asn His Pro Ile Phe Tyr Lys Asn
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 Ser Ile Lys Leu Gly Tyr Val Ile Arg Ser Ile Asp Val Phe Asn Ser
 450 455 460
 Gln Ile Leu His Thr Ser Arg Gln Leu Ser Leu Asn His Tyr Leu Leu
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 Pro Pro Asp Ser Phe Ala Val Tyr Arg Ile Ile Asp Ser Asn Gly Ser
 485 490 495
 Trp Phe Asp Ile Gly Ile Asp Ser Asp Gly Phe Ser Phe Val Gly Val
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 Ser Gly Phe Gly Lys Leu Glu Phe Pro Leu Ser Ala Ser Tyr Met Gly
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<220>
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 <222> (1)..(1752)

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 Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly Gly Gly
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 Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe Asn Asn Gln
 35 40 45
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 Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn
 50 55 60
 tca agc aga ctt gta cat tta aat atg cca gaa agt gaa aat tat aaa 240
 Ser Ser Arg Leu Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Lys

65	70	75	80	
aga gta gtt gta aat aat atg gat aaa act gca gtt aaa gga aac atg				288
Arg Val Val Val Asn Asn Met Asp Lys Thr Ala Val Lys Gly Asn Met	85	90	95	
gct tta gat gat att cat gta caa att gta aca cct tgg tca ttg gtt				336
Ala Leu Asp Asp Ile His Val Gln Ile Val Thr Pro Trp Ser Leu Val	100	105	110	
gat gca aat gct tgg gga gtt tgg ttt aat cca gga gat tgg caa cta				384
Asp Ala Asn Ala Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu	115	120	125	
att gtt aat act atg agt gag ttg cat tta gtt agt ttt gaa caa gaa				432
Ile Val Asn Thr Met Ser Glu Leu His Leu Val Ser Phe Glu Gln Glu	130	135	140	
att ttt aat gtt gtt tta aag act gtt tca gaa tct gct act cag cca				480
Ile Phe Asn Val Val Leu Lys Thr Val Ser Glu Ser Ala Thr Gln Pro	145	150	155	160
cca act aaa gtt tat aat aat gat tta act gca tca ttg atg gtt gca				528
Pro Thr Lys Val Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala	165	170	175	
tta gat agt aat aat act atg cca ttt act cca gca gct atg aga tct				576
Leu Asp Ser Asn Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser	180	185	190	
gag aca ttg ggt ttt tat cca tgg aaa cca acc ata cca act cca tgg				624
Glu Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp	195	200	205	
aga tat tat ttt caa tgg gat aga aca tta ata cca tct cat act gga				672
Arg Tyr Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly	210	215	220	
act agt ggc aca cca aca aat gta tat cat ggt aca gat cca gat gat				720
Thr Ser Gly Thr Pro Thr Asn Val Tyr His Gly Thr Asp Pro Asp Asp	225	230	235	240
gtt caa ttt tat act att gaa aat tct gtg cca gta cac tta cta aga				768
Val Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu Arg	245	250	255	
aca ggt gat gaa ttt gct aca gga aca ttt ttt ttt gat tgt aaa cca				816
Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys Lys Pro	260	265	270	
tgt aga tta aca cat aca tgg caa aca aat aga gca ttg ggc tta cca				864
Cys Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu Gly Leu Pro	275	280	285	
cca ttt tta aat tct ttg cct caa tct gaa gga gct act aac ttt ggt				912
Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala Thr Asn Phe Gly	290	295	300	

gat ata gga gtt caa caa gat aaa aga cgt ggt gta act caa atg gga Asp Ile Gly Val Gln Gln Asp Lys Arg Arg Gly Val Thr Gln Met Gly 305 310 315 320	960
aat aca gac tat att act gaa gct act att atg aga cca gct gag gtt Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile Met Arg Pro Ala Glu Val 325 330 335	1008
ggt tat agt gca cca tat tat tct ttt gaa gcg tct aca caa ggg cca Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe Glu Ala Ser Thr Gln Gly Pro 340 345 350	1056
ttt aaa aca cct att gca gca gga cgg ggg gga gcg caa aca gat gaa Phe Lys Thr Pro Ile Ala Ala Gly Arg Gly Gly Ala Gln Thr Asp Glu 355 360 365	1104
aat caa gca gca gat ggt gat cca aga tat gca ttt ggt aga caa cat Asn Gln Ala Ala Asp Gly Asp Pro Arg Tyr Ala Phe Gly Arg Gln His 370 375 380	1152
ggt caa aaa act act aca aca gga gaa aca cct gag aga ttt aca tat Gly Gln Lys Thr Thr Thr Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr 385 390 395 400	1200
ata gca cat caa gat aca gga aga tat cca gaa gga gat tgg att caa Ile Ala His Gln Asp Thr Gly Arg Tyr Pro Glu Gly Asp Trp Ile Gln 405 410 415	1248
aat att aac ttt aac ctt cct gta aca aat gat aat gta ttg cta cca Asn Ile Asn Phe Asn Leu Pro Val Thr Asn Asp Asn Val Leu Leu Pro 420 425 430	1296
aca gat cca att ggg ggt aaa aca gga att aac tat act aat ata ttt Thr Asp Pro Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe 435 440 445	1344
aat act tat ggt cct tta act gca tta aat aat gta cca cca gtt tat Asn Thr Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr 450 455 460	1392
cca aat ggt caa att tgg gat aaa gaa ttt gat act gac tta aaa cca Pro Asn Gly Gln Ile Trp Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro 465 470 475 480	1440
aga ctt cat gta aat gca cca ttt gtt tgt caa aat aat tgt cct ggt Arg Leu His Val Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro Gly 485 490 495	1488
caa tta ttt gta aaa gtt gcg cct aat tta acg aat gaa tat gat cct Gln Leu Phe Val Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr Asp Pro 500 505 510	1536
gat gca tct gct aat atg tca aga att gta act tat tca gat ttt tgg Asp Ala Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser Asp Phe Trp 515 520 525	1584

tgg aaa ggt aaa tta gta ttt aaa gct aaa cta aga gca tct cat act	1632
Trp Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg Ala Ser His Thr	
530 535 540	
tgg aat cca att caa caa atg agc att aat gta gat aac caa ttt aac	1680
Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val Asp Asn Gln Phe Asn	
545 550 555 560	
tat gta cca aat aat att gga gct atg aaa att gta tat gaa aaa tct	1728
Tyr Val Pro Asn Asn Ile Gly Ala Met Lys Ile Val Tyr Glu Lys Ser	
565 570 575	
caa cta gca cct aga aaa tta tat	1752
Gln Leu Ala Pro Arg Lys Leu Tyr	
580	
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Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly Gly Gly	
20 25 30	
Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe Asn Asn Gln	
35 40 45	
Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn	
50 55 60	
Ser Ser Arg Leu Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Lys	
65 70 75 80	
Arg Val Val Val Asn Asn Met Asp Lys Thr Ala Val Lys Gly Asn Met	
85 90 95	
Ala Leu Asp Asp Ile His Val Gln Ile Val Thr Pro Trp Ser Leu Val	
100 105 110	
Asp Ala Asn Ala Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu	
115 120 125	
Ile Val Asn Thr Met Ser Glu Leu His Leu Val Ser Phe Glu Gln Glu	
130 135 140	
Ile Phe Asn Val Val Leu Lys Thr Val Ser Glu Ser Ala Thr Gln Pro	
145 150 155 160	
Pro Thr Lys Val Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala	
165 170 175	
Leu Asp Ser Asn Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser	

180						185						190					
Glu	Thr	Leu	Gly	Phe	Tyr	Pro	Trp	Lys	Pro	Thr	Ile	Pro	Thr	Pro	Trp		
		195					200					205					
Arg	Tyr	Tyr	Phe	Gln	Trp	Asp	Arg	Thr	Leu	Ile	Pro	Ser	His	Thr	Gly		
	210					215					220						
Thr	Ser	Gly	Thr	Pro	Thr	Asn	Val	Tyr	His	Gly	Thr	Asp	Pro	Asp	Asp		
225					230					235					240		
Val	Gln	Phe	Tyr	Thr	Ile	Glu	Asn	Ser	Val	Pro	Val	His	Leu	Leu	Arg		
				245					250					255			
Thr	Gly	Asp	Glu	Phe	Ala	Thr	Gly	Thr	Phe	Phe	Phe	Asp	Cys	Lys	Pro		
			260					265					270				
Cys	Arg	Leu	Thr	His	Thr	Trp	Gln	Thr	Asn	Arg	Ala	Leu	Gly	Leu	Pro		
		275					280					285					
Pro	Phe	Leu	Asn	Ser	Leu	Pro	Gln	Ser	Glu	Gly	Ala	Thr	Asn	Phe	Gly		
	290					295					300						
Asp	Ile	Gly	Val	Gln	Gln	Asp	Lys	Arg	Arg	Gly	Val	Thr	Gln	Met	Gly		
305					310					315					320		
Asn	Thr	Asp	Tyr	Ile	Thr	Glu	Ala	Thr	Ile	Met	Arg	Pro	Ala	Glu	Val		
				325					330					335			
Gly	Tyr	Ser	Ala	Pro	Tyr	Tyr	Ser	Phe	Glu	Ala	Ser	Thr	Gln	Gly	Pro		
			340					345					350				
Phe	Lys	Thr	Pro	Ile	Ala	Ala	Gly	Arg	Gly	Gly	Ala	Gln	Thr	Asp	Glu		
		355					360					365					
Asn	Gln	Ala	Ala	Asp	Gly	Asp	Pro	Arg	Tyr	Ala	Phe	Gly	Arg	Gln	His		
	370					375					380						
Gly	Gln	Lys	Thr	Thr	Thr	Thr	Gly	Glu	Thr	Pro	Glu	Arg	Phe	Thr	Tyr		
385					390					395					400		
Ile	Ala	His	Gln	Asp	Thr	Gly	Arg	Tyr	Pro	Glu	Gly	Asp	Trp	Ile	Gln		
				405					410					415			
Asn	Ile	Asn	Phe	Asn	Leu	Pro	Val	Thr	Asn	Asp	Asn	Val	Leu	Leu	Pro		
			420					425					430				
Thr	Asp	Pro	Ile	Gly	Gly	Lys	Thr	Gly	Ile	Asn	Tyr	Thr	Asn	Ile	Phe		
		435					440					445					
Asn	Thr	Tyr	Gly	Pro	Leu	Thr	Ala	Leu	Asn	Asn	Val	Pro	Pro	Val	Tyr		
	450					455					460						
Pro	Asn	Gly	Gln	Ile	Trp	Asp	Lys	Glu	Phe	Asp	Thr	Asp	Leu	Lys	Pro		
465					470					475					480		
Arg	Leu	His	Val	Asn	Ala	Pro	Phe	Val	Cys	Gln	Asn	Asn	Cys	Pro	Gly		

485	490	495
Gln Leu Phe Val Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr Asp Pro		
500	505	510
Asp Ala Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser Asp Phe Trp		
515	520	525
Trp Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg Ala Ser His Thr		
530	535	540
Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val Asp Asn Gln Phe Asn		
545	550	555
		560
Tyr Val Pro Asn Asn Ile Gly Ala Met Lys Ile Val Tyr Glu Lys Ser		
565	570	575
Gln Leu Ala Pro Arg Lys Leu Tyr		
580		

<210> 7
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 <212> DNA
 <213> Feline parvovirus

<220>
 <221> CDS
 <222> (1)..(729)

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Gly Thr Asp Pro Asp Asp Val Gln Phe Tyr Thr Ile Glu Asn Ser Val		
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		15
cca gta cac tta cta aga aca ggt gat gaa ttt gct aca gga aca ttt		96
Pro Val His Leu Leu Arg Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe		
20	25	30
ttt ttt gat tgt aaa cca tgt aga tta aca cat aca tgg caa aca aat		144
Phe Phe Asp Cys Lys Pro Cys Arg Leu Thr His Thr Trp Gln Thr Asn		
35	40	45
aga gca ttg ggc tta cca cca ttt tta aat tct ttg cct caa tct gaa		192
Arg Ala Leu Gly Leu Pro Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu		
50	55	60
gga gct act aac ttt ggt gat ata gga gtt caa caa gat aaa aga cgt		240
Gly Ala Thr Asn Phe Gly Asp Ile Gly Val Gln Gln Asp Lys Arg Arg		
65	70	75
		80
ggt gta act caa atg gga aat aca gac tat att act gaa gct act att		288
Gly Val Thr Gln Met Gly Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile		
85	90	95
atg aga cca gct gag gtt ggt tat agt gca cca tat tat tct ttt gaa		336

Met	Arg	Pro	Ala	Glu	Val	Gly	Tyr	Ser	Ala	Pro	Tyr	Tyr	Ser	Phe	Glu		
			100					105					110				
gcg	tct	aca	caa	ggg	cca	ttt	aaa	aca	cct	att	gca	gca	gga	cgg	ggg	384	
Ala	Ser	Thr	Gln	Gly	Pro	Phe	Lys	Thr	Pro	Ile	Ala	Ala	Gly	Arg	Gly		
		115					120					125					
gga	gcg	caa	aca	gat	gaa	aat	caa	gca	gca	gat	ggt	gat	cca	aga	tat	432	
Gly	Ala	Gln	Thr	Asp	Glu	Asn	Gln	Ala	Ala	Asp	Gly	Asp	Pro	Arg	Tyr		
		130				135					140						
gca	ttt	ggt	aga	caa	cat	ggt	caa	aaa	act	act	aca	aca	gga	gaa	aca	480	
Ala	Phe	Gly	Arg	Gln	His	Gly	Gln	Lys	Thr	Thr	Thr	Thr	Gly	Glu	Thr		
145					150				155						160		
cct	gag	aga	ttt	aca	tat	ata	gca	cat	caa	gat	aca	gga	aga	tat	cca	528	
Pro	Glu	Arg	Phe	Thr	Tyr	Ile	Ala	His	Gln	Asp	Thr	Gly	Arg	Tyr	Pro		
			165						170					175			
gaa	gga	gat	tgg	att	caa	aat	att	aac	ttt	aac	ctt	cct	gta	aca	aat	576	
Glu	Gly	Asp	Trp	Ile	Gln	Asn	Ile	Asn	Phe	Asn	Leu	Pro	Val	Thr	Asn		
		180						185					190				
gat	aat	gta	ttg	cta	cca	aca	gat	cca	att	ggg	ggt	aaa	aca	gga	att	624	
Asp	Asn	Val	Leu	Leu	Pro	Thr	Asp	Pro	Ile	Gly	Gly	Lys	Thr	Gly	Ile		
		195					200					205					
aac	tat	act	aat	ata	ttt	aat	act	tat	ggt	cct	tta	act	gca	tta	aat	672	
Asn	Tyr	Thr	Asn	Ile	Phe	Asn	Thr	Tyr	Gly	Pro	Leu	Thr	Ala	Leu	Asn		
	210					215					220						
aat	gta	cca	cca	gtt	tat	cca	aat	ggt	caa	att	tgg	gat	aaa	gaa	ttt	720	
Asn	Val	Pro	Pro	Val	Tyr	Pro	Asn	Gly	Gln	Ile	Trp	Asp	Lys	Glu	Phe		
225					230				235					240			
gat	act	gac														729	
Asp	Thr	Asp															

<210> 8

<211> 243

<212> PRT

<213> Feline parvovirus

<400> 8

Gly	Thr	Asp	Pro	Asp	Asp	Val	Gln	Phe	Tyr	Thr	Ile	Glu	Asn	Ser	Val
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Pro	Val	His	Leu	Leu	Arg	Thr	Gly	Asp	Glu	Phe	Ala	Thr	Gly	Thr	Phe
		20					25						30		

Phe	Phe	Asp	Cys	Lys	Pro	Cys	Arg	Leu	Thr	His	Thr	Trp	Gln	Thr	Asn
		35				40						45			

Arg	Ala	Leu	Gly	Leu	Pro	Pro	Phe	Leu	Asn	Ser	Leu	Pro	Gln	Ser	Glu
	50					55					60				

Gly	Ala	Thr	Asn	Phe	Gly	Asp	Ile	Gly	Val	Gln	Gln	Asp	Lys	Arg	Arg	
65					70					75					80	
Gly	Val	Thr	Gln	Met	Gly	Asn	Thr	Asp	Tyr	Ile	Thr	Glu	Ala	Thr	Ile	
				85					90						95	
Met	Arg	Pro	Ala	Glu	Val	Gly	Tyr	Ser	Ala	Pro	Tyr	Tyr	Ser	Phe	Glu	
			100					105					110			
Ala	Ser	Thr	Gln	Gly	Pro	Phe	Lys	Thr	Pro	Ile	Ala	Ala	Gly	Arg	Gly	
		115					120					125				
Gly	Ala	Gln	Thr	Asp	Glu	Asn	Gln	Ala	Ala	Asp	Gly	Asp	Pro	Arg	Tyr	
130						135					140					
Ala	Phe	Gly	Arg	Gln	His	Gly	Gln	Lys	Thr	Thr	Thr	Thr	Gly	Glu	Thr	
145					150					155					160	
Pro	Glu	Arg	Phe	Thr	Tyr	Ile	Ala	His	Gln	Asp	Thr	Gly	Arg	Tyr	Pro	
				165					170					175		
Glu	Gly	Asp	Trp	Ile	Gln	Asn	Ile	Asn	Phe	Asn	Leu	Pro	Val	Thr	Asn	
		180					185						190			
Asp	Asn	Val	Leu	Leu	Pro	Thr	Asp	Pro	Ile	Gly	Gly	Lys	Thr	Gly	Ile	
		195					200					205				
Asn	Tyr	Thr	Asn	Ile	Phe	Asn	Thr	Tyr	Gly	Pro	Leu	Thr	Ala	Leu	Asn	
210					215						220					
Asn	Val	Pro	Pro	Val	Tyr	Pro	Asn	Gly	Gln	Ile	Trp	Asp	Lys	Glu	Phe	
225					230					235					240	
Asp	Thr	Asp														

<210> 9
 <211> 1860
 <212> DNA
 <213> Feline parvovirus

<220>
 <221> CDS
 <222> (1)..(1860)

<400> 9																
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Met	Ala	Pro	Pro	Ala	Lys	Arg	Ala	Arg	Arg	Gly	Leu	Val	Pro	Pro	Gly	
1				5				10					15			
tat	aaa	tat	ctt	ggg	cct	ggg	aac	agt	ctt	gac	caa	gga	gaa	cca	act	96
Tyr	Lys	Tyr	Leu	Gly	Pro	Gly	Asn	Ser	Leu	Asp	Gln	Gly	Glu	Pro	Thr	
			20				25					30				
aac	cct	tct	gac	gcc	gct	gca	aaa	gaa	cac	gac	gaa	gct	tac	gct	gct	144

Asn Pro Ser Asp Ala Ala Ala Lys Glu His Asp Glu Ala Tyr Ala Ala	
35 40 45	
tat ctt cgc tct ggt aaa aac cca tac tta tat ttc tcg cca gca gat	192
Tyr Leu Arg Ser Gly Lys Asn Pro Tyr Leu Tyr Phe Ser Pro Ala Asp	
50 55 60	
caa cgc ttt ata gat caa act aag gac gct aca gat tgg ggg ggg aaa	240
Gln Arg Phe Ile Asp Gln Thr Lys Asp Ala Thr Asp Trp Gly Gly Lys	
65 70 75 80	
ata gga cat tat ttt ttt aga gct aaa aaa gca att gct cca gta tta	288
Ile Gly His Tyr Phe Phe Arg Ala Lys Lys Ala Ile Ala Pro Val Leu	
85 90 95	
act gat aca cca gat cat cca tca aca tca aga cca aca aaa cca act	336
Thr Asp Thr Pro Asp His Pro Ser Thr Ser Arg Pro Thr Lys Pro Thr	
100 105 110	
aaa aga agt aaa cca cca cct cat att ttc atc aat ctt gca aaa aaa	384
Lys Arg Ser Lys Pro Pro Pro His Ile Phe Ile Asn Leu Ala Lys Lys	
115 120 125	
aaa aaa gcc ggt gca gga caa gta aaa aga gac aat caa gca cca atg	432
Lys Lys Ala Gly Ala Gly Gln Val Lys Arg Asp Asn Gln Ala Pro Met	
130 135 140	
agt gat gga gca gtt caa cca gac ggt ggt caa cct gct gtc aga aat	480
Ser Asp Gly Ala Val Gln Pro Asp Gly Gly Gln Pro Ala Val Arg Asn	
145 150 155 160	
gaa aga gct aca gga tct ggg aac ggg tct gga ggc ggg ggt ggt ggt	528
Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly Gly Gly Gly	
165 170 175	
ggt tct ggg ggt gtg ggg att tct acg ggt act ttc aat aat cag acg	576
Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe Asn Asn Gln Thr	
180 185 190	
gaa ttt aaa ttt ttg gaa aac gga tgg gtg gaa atc aca gca aac tca	624
Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn Ser	
195 200 205	
agc aga ctt gta cat tta aat atg cca gaa agt gaa aat tat aaa aga	672
Ser Arg Leu Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Lys Arg	
210 215 220	
gta gtt gta aat aat atg gat aaa act gca gtt aaa gga aac atg gct	720
Val Val Val Asn Asn Met Asp Lys Thr Ala Val Lys Gly Asn Met Ala	
225 230 235 240	
tta gat gac act cat gta caa att gta aca cct tgg tca ttg gtt gat	768
Leu Asp Asp Thr His Val Gln Ile Val Thr Pro Trp Ser Leu Val Asp	
245 250 255	
gca aat gct tgg gga gtt tgg ttt aat cca gga gat tgg caa cta att	816
Ala Asn Ala Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu Ile	

260	265	270	
gtt aat act atg agt gag ttg cat tta gtt agt ttt gaa caa gaa att Val Asn Thr Met Ser Glu Leu His Leu Val Ser Phe Glu Gln Glu Ile 275 280 285			864
ttt aat gtt gtt tta aag act gtt tca gaa tct gct act cag cca cca Phe Asn Val Val Leu Lys Thr Val Ser Glu Ser Ala Thr Gln Pro Pro 290 295 300			912
act aaa gtt tat aat aat gat tta act gca tca ttg atg gtt gca tta Thr Lys Val Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala Leu 305 310 315 320			960
gat agt aat aat act atg cca ttt act cca gca gct atg aga tct gag Asp Ser Asn Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser Glu 325 330 335			1008
aca ttg ggt ttt tat cca tgg aaa cca acc ata cca act cca tgg aga Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp Arg 340 345 350			1056
tat tat ttt caa tgg gat aga aca tta ata cca tct cat act gga act Tyr Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly Thr 355 360 365			1104
agt ggc aca cca aca aat ata tat cat ggt aca gat cca gat gat gtt Ser Gly Thr Pro Thr Asn Ile Tyr His Gly Thr Asp Pro Asp Asp Val 370 375 380			1152
caa ttt tat act att gaa aat tct gtg cca gta cac tta cta aga aca Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu Arg Thr 385 390 395 400			1200
ggt gat gaa ttt gct aca gga aca ttt ttt ttt gat tgt aaa cca tgt Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys Lys Pro Cys 405 410 415			1248
aga cta aca cat aca tgg caa aca aac aga gca ttg ggc tta cca cca Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu Gly Leu Pro Pro 420 425 430			1296
ttt cta aat tct ttg cct caa tct gaa gga gct act aac ttt ggt gat Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala Thr Asn Phe Gly Asp 435 440 445			1344
ata gga gtt caa caa gat aaa aga cgt ggt gta act caa atg gga aat Ile Gly Val Gln Gln Asp Lys Arg Arg Gly Val Thr Gln Met Gly Asn 450 455 460			1392
aca gac tat att act gaa gct act att atg aga cca gct gag gtt ggt Thr Asp Tyr Ile Thr Glu Ala Thr Ile Met Arg Pro Ala Glu Val Gly 465 470 475 480			1440
tat agt gca cca tat tat tct ttt gaa gcg tct aca caa ggg cca ttt Tyr Ser Ala Pro Tyr Tyr Ser Phe Glu Ala Ser Thr Gln Gly Pro Phe 485 490 495			1488

aaa ata cct att gca gca gga cgg ggg gga gcg caa aca gat gaa aat	1536
Lys Ile Pro Ile Ala Ala Gly Arg Gly Gly Ala Gln Thr Asp Glu Asn	
500 505 510	
caa gca gca gat ggt gat cca aga tat gca ttt ggt aga caa cat ggt	1584
Gln Ala Ala Asp Gly Asp Pro Arg Tyr Ala Phe Gly Arg Gln His Gly	
515 520 525	
caa aaa act act aca aca gga gaa aca cct gag aga ttt aca tat ata	1632
Gln Lys Thr Thr Thr Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr Ile	
530 535 540	
gca cat caa gat aca gga aga tat cca gca gga gat tgg att caa aat	1680
Ala His Gln Asp Thr Gly Arg Tyr Pro Ala Gly Asp Trp Ile Gln Asn	
545 550 555 560	
att aac ttt aac ctt cct gta aca aat gat aat gta ttg cta cca aca	1728
Ile Asn Phe Asn Leu Pro Val Thr Asn Asp Asn Val Leu Leu Pro Thr	
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gat cca att gga ggt aaa aca gga atc aac tat act aat ata ttt aat	1776
Asp Pro Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe Asn	
580 585 590	
act tat ggt cct tta act gca tta aat aat gta cca cca gtt tat cca	1824
Thr Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr Pro	
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35 40 45	
Tyr Leu Arg Ser Gly Lys Asn Pro Tyr Leu Tyr Phe Ser Pro Ala Asp	
50 55 60	
Gln Arg Phe Ile Asp Gln Thr Lys Asp Ala Thr Asp Trp Gly Gly Lys	
65 70 75 80	
Ile Gly His Tyr Phe Phe Arg Ala Lys Lys Ala Ile Ala Pro Val Leu	
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Thr Asp Thr Pro Asp His Pro Ser Thr Ser Arg Pro Thr Lys Pro Thr
 100 105 110
 Lys Arg Ser Lys Pro Pro Pro His Ile Phe Ile Asn Leu Ala Lys Lys
 115 120 125
 Lys Lys Ala Gly Ala Gly Gln Val Lys Arg Asp Asn Gln Ala Pro Met
 130 135 140
 Ser Asp Gly Ala Val Gln Pro Asp Gly Gly Gln Pro Ala Val Arg Asn
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 Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly Gly Gly Gly
 165 170 175
 Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe Asn Asn Gln Thr
 180 185 190
 Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn Ser
 195 200 205
 Ser Arg Leu Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Lys Arg
 210 215 220
 Val Val Val Asn Asn Met Asp Lys Thr Ala Val Lys Gly Asn Met Ala
 225 230 235 240
 Leu Asp Asp Thr His Val Gln Ile Val Thr Pro Trp Ser Leu Val Asp
 245 250 255
 Ala Asn Ala Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu Ile
 260 265 270
 Val Asn Thr Met Ser Glu Leu His Leu Val Ser Phe Glu Gln Glu Ile
 275 280 285
 Phe Asn Val Val Leu Lys Thr Val Ser Glu Ser Ala Thr Gln Pro Pro
 290 295 300
 Thr Lys Val Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala Leu
 305 310 315 320
 Asp Ser Asn Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser Glu
 325 330 335
 Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp Arg
 340 345 350
 Tyr Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly Thr
 355 360 365
 Ser Gly Thr Pro Thr Asn Ile Tyr His Gly Thr Asp Pro Asp Asp Val
 370 375 380
 Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu Arg Thr
 385 390 395 400

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aat gaa aga gct aca gga tct ggg aac ggg tct gga ggc ggg ggt ggt	Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly Gly Gly	96		
	20	25	30	
ggg ggt tct ggg ggt gtg ggg att tct acg ggt act ttc aat aat cag	Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe Asn Asn Gln	144		
	35	40	45	
acg gaa ttt aaa ttt ttg gaa aac gga tgg gtg gaa atc aca gca aac	Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn	192		
	50	55	60	
tca agc aga ctt gta cat tta aat atg cca gaa agt gaa aat tat aaa	Ser Ser Arg Leu Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Lys	240		
	65	70	75	80
aga gta gtt gta aat aat atg gat aaa act gca gtt aaa gga aac atg	Arg Val Val Val Asn Asn Met Asp Lys Thr Ala Val Lys Gly Asn Met	288		
	85	90	95	
gct tta gat gac act cat gta caa att gta aca cct tgg tca ttg gtt	Ala Leu Asp Asp Thr His Val Gln Ile Val Thr Pro Trp Ser Leu Val	336		
	100	105	110	
gat gca aat gct tgg gga gtt tgg ttt aat cca gga gat tgg caa cta	Asp Ala Asn Ala Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu	384		
	115	120	125	
att gtt aat act atg agt gag ttg cat tta gtt agt ttt gaa caa gaa	Ile Val Asn Thr Met Ser Glu Leu His Leu Val Ser Phe Glu Gln Glu	432		
	130	135	140	
att ttt aat gtt gtt tta aag act gtt tca gaa tct gct act cag cca	Ile Phe Asn Val Val Leu Lys Thr Val Ser Glu Ser Ala Thr Gln Pro	480		
	145	150	155	160
cca act aaa gtt tat aat aat gat tta act gca tca ttg atg gtt gca	Pro Thr Lys Val Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala	528		
	165	170	175	
tta gat agt aat aat act atg cca ttt act cca gca gct atg aga tct	Leu Asp Ser Asn Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser	576		
	180	185	190	
gag aca ttg ggt ttt tat cca tgg aaa cca acc ata cca act cca tgg	Glu Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp	624		
	195	200	205	
aga tat tat ttt caa tgg gat aga aca tta ata cca tct cat act gga	Arg Tyr Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly	672		
	210	215	220	
act agt ggc aca cca aca aat ata tat cat ggt aca gat cca gat gat	Thr Ser Gly Thr Pro Thr Asn Ile Tyr His Gly Thr Asp Pro Asp Asp	720		
	225	230	235	240

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aca ggt gat gaa ttt gct aca gga aca ttt ttt ttt gat tgt aaa cca Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys Lys Pro 260 265 270	816
tgt aga cta aca cat aca tgg caa aca aac aga gca ttg ggc tta cca Cys Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu Gly Leu Pro 275 280 285	864
cca ttt cta aat tct ttg cct caa tct gaa gga gct act aac ttt ggt Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala Thr Asn Phe Gly 290 295 300	912
gat ata gga gtt caa caa gat aaa aga cgt ggt gta act caa atg gga Asp Ile Gly Val Gln Gln Asp Lys Arg Arg Gly Val Thr Gln Met Gly 305 310 315 320	960
aat aca gac tat att act gaa gct act att atg aga cca gct gag gtt Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile Met Arg Pro Ala Glu Val 325 330 335	1008
ggt tat agt gca cca tat tat tct ttt gaa gcg tct aca caa ggg cca Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe Glu Ala Ser Thr Gln Gly Pro 340 345 350	1056
ttt aaa ata cct att gca gca gga cgg ggg gga gcg caa aca gat gaa Phe Lys Ile Pro Ile Ala Ala Gly Arg Gly Gly Ala Gln Thr Asp Glu 355 360 365	1104
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ggt caa aaa act act aca aca gga gaa aca cct gag aga ttt aca tat Gly Gln Lys Thr Thr Thr Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr 385 390 395 400	1200
ata gca cat caa gat aca gga aga tat cca gca gga gat tgg att caa Ile Ala His Gln Asp Thr Gly Arg Tyr Pro Ala Gly Asp Trp Ile Gln 405 410 415	1248
aat att aac ttt aac ctt cct gta aca aat gat aat gta ttg cta cca Asn Ile Asn Phe Asn Leu Pro Val Thr Asn Asp Asn Val Leu Leu Pro 420 425 430	1296
aca gat cca att gga ggt aaa aca gga atc aac tat act aat ata ttt Thr Asp Pro Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe 435 440 445	1344
aat act tat ggt cct tta act gca tta aat aat gta cca cca gtt tat Asn Thr Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr 450 455 460	1392

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1431

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 35 40 45
 Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn
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 Ser Ser Arg Leu Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Lys
 65 70 75 80
 Arg Val Val Val Asn Asn Met Asp Lys Thr Ala Val Lys Gly Asn Met
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 Ala Leu Asp Asp Thr His Val Gln Ile Val Thr Pro Trp Ser Leu Val
 100 105 110
 Asp Ala Asn Ala Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu
 115 120 125
 Ile Val Asn Thr Met Ser Glu Leu His Leu Val Ser Phe Glu Gln Glu
 130 135 140
 Ile Phe Asn Val Val Leu Lys Thr Val Ser Glu Ser Ala Thr Gln Pro
 145 150 155 160
 Pro Thr Lys Val Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala
 165 170 175
 Leu Asp Ser Asn Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser
 180 185 190
 Glu Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp
 195 200 205
 Arg Tyr Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly
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 Thr Ser Gly Thr Pro Thr Asn Ile Tyr His Gly Thr Asp Pro Asp Asp
 225 230 235 240
 Val Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu Arg

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Thr	Gly	Asp	Glu	Phe	Ala	Thr	Gly	Thr	Phe	Phe	Phe	Phe	Asp	Cys	Lys	Pro			
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Cys	Arg	Leu	Thr	His	Thr	Trp	Gln	Thr	Asn	Arg	Ala	Leu	Gly	Leu	Pro				
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Pro	Phe	Leu	Asn	Ser	Leu	Pro	Gln	Ser	Glu	Gly	Ala	Thr	Asn	Phe	Gly				
		290				295					300								
Asp	Ile	Gly	Val	Gln	Gln	Asp	Lys	Arg	Arg	Gly	Val	Thr	Gln	Met	Gly				
305				310						315					320				
Asn	Thr	Asp	Tyr	Ile	Thr	Glu	Ala	Thr	Ile	Met	Arg	Pro	Ala	Glu	Val				
			325						330					335					
Gly	Tyr	Ser	Ala	Pro	Tyr	Tyr	Ser	Phe	Glu	Ala	Ser	Thr	Gln	Gly	Pro				
			340					345					350						
Phe	Lys	Ile	Pro	Ile	Ala	Ala	Gly	Arg	Gly	Gly	Ala	Gln	Thr	Asp	Glu				
		355					360					365							
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Gly	Gln	Lys	Thr	Thr	Thr	Thr	Gly	Glu	Thr	Pro	Glu	Arg	Phe	Thr	Tyr				
385					390				395						400				
Ile	Ala	His	Gln	Asp	Thr	Gly	Arg	Tyr	Pro	Ala	Gly	Asp	Trp	Ile	Gln				
			405					410						415					
Asn	Ile	Asn	Phe	Asn	Leu	Pro	Val	Thr	Asn	Asp	Asn	Val	Leu	Leu	Pro				
		420					425					430							
Thr	Asp	Pro	Ile	Gly	Gly	Lys	Thr	Gly	Ile	Asn	Tyr	Thr	Asn	Ile	Phe				
		435					440					445							
Asn	Thr	Tyr	Gly	Pro	Leu	Thr	Ala	Leu	Asn	Asn	Val	Pro	Pro	Val	Tyr				
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Pro	Asn	Gly	Gln	Ile	Trp	Asp	Lys	Glu	Phe	Asp	Thr	Asp							
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<212> DNA

<213> Feline herpesvirus 1

<220>

<221> CDS

<222> (1)..(2829)

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Gln	Gly	His	Ser	Gly	Tyr	Phe	Arg	Gln	Arg	Cys	Phe	Phe	Pro	Ser	Leu	
			20					25					30			
ctc	ggt	att	gca	gcg	act	ggc	tcc	aga	cat	ggt	aac	gga	tcg	tcg	gga	144
Leu	Gly	Ile	Ala	Ala	Thr	Gly	Ser	Arg	His	Gly	Asn	Gly	Ser	Ser	Gly	
		35					40					45				
tta	acc	aga	cta	gct	aga	tat	gtt	tca	ttt	atc	tgg	atc	gta	cta	ttc	192
Leu	Thr	Arg	Leu	Ala	Arg	Tyr	Val	Ser	Phe	Ile	Trp	Ile	Val	Leu	Phe	
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tta	gtc	ggt	ccc	cgt	cca	gta	gag	ggt	caa	tct	gga	agc	aca	tcg	gaa	240
Leu	Val	Gly	Pro	Arg	Pro	Val	Glu	Gly	Gln	Ser	Gly	Ser	Thr	Ser	Glu	
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caa	ccc	cgg	cgg	act	gta	gct	acc	cct	gag	gta	ggg	gta	cac	cac	caa	288
Gln	Pro	Arg	Arg	Thr	Val	Ala	Thr	Pro	Glu	Val	Gly	Val	His	His	Gln	
				85					90					95		
aac	caa	cta	cag	atc	cca	ccg	ata	tgt	cga	tat	gag	gaa	gct	ctc	cgt	336
Asn	Gln	Leu	Gln	Ile	Pro	Pro	Ile	Cys	Arg	Tyr	Glu	Glu	Ala	Leu	Arg	
		100						105					110			
gcg	tcc	caa	ata	gag	gct	aac	gga	cca	tcg	act	ttt	tat	atg	tgt	cca	384
Ala	Ser	Gln	Ile	Glu	Ala	Asn	Gly	Pro	Ser	Thr	Phe	Tyr	Met	Cys	Pro	
		115					120					125				
cca	cct	tca	gga	tct	act	gtc	gtg	cgt	tta	gag	cca	cca	cgg	gcc	tgt	432
Pro	Pro	Ser	Gly	Ser	Thr	Val	Val	Arg	Leu	Glu	Pro	Pro	Arg	Ala	Cys	
	130					135					140					
cca	gat	tat	aaa	cta	ggg	aaa	aat	ttt	acc	gag	ggt	ata	gct	gta	ata	480
Pro	Asp	Tyr	Lys	Leu	Gly	Lys	Asn	Phe	Thr	Glu	Gly	Ile	Ala	Val	Ile	
145					150					155					160	
ttt	aaa	gaa	aat	ata	gcg	cca	tat	aaa	ttc	aag	gca	aat	ata	tac	tat	528
Phe	Lys	Glu	Asn	Ile	Ala	Pro	Tyr	Lys	Phe	Lys	Ala	Asn	Ile	Tyr	Tyr	
				165				170					175			
aaa	aac	att	att	atg	aca	acg	gta	tgg	tct	ggg	agt	tcc	tat	gcc	gtt	576
Lys	Asn	Ile	Ile	Met	Thr	Thr	Val	Trp	Ser	Gly	Ser	Ser	Tyr	Ala	Val	
		180						185					190			
aca	acc	aac	cga	tat	aca	gac	agg	gtt	ccc	gtg	aaa	gtt	caa	gag	att	624
Thr	Thr	Asn	Arg	Tyr	Thr	Asp	Arg	Val	Pro	Val	Lys	Val	Gln	Glu	Ile	
		195					200					205				
aca	gat	ctc	ata	gat	aga	cgg	ggt	atg	tgc	ctc	tcg	aaa	gct	gat	tac	672
Thr	Asp	Leu	Ile	Asp	Arg	Arg	Gly	Met	Cys	Leu	Ser	Lys	Ala	Asp	Tyr	
	210					215					220					
gtt	cgt	aac	aat	tat	caa	ttt	acg	gcc	ttt	gat	cga	gac	gag	gat	ccc	720
Val	Arg	Asn	Asn	Tyr	Gln	Phe	Thr	Ala	Phe	Asp	Arg	Asp	Glu	Asp	Pro	

225	230	235	240	
aga gaa ctg cct ctg	aaa cct cca agt	tca aca ctc tcc	aga gtc cgt	768
Arg Glu Leu Pro	Leu Lys Pro Pro	Ser Ser Thr Leu	Ser Arg Val Arg	
	245	250	255	
gga tgg cac acc aat	gaa aca tac aca	aag atc gtg ctg	ctg gat ttc	816
Gly Trp His Thr	Asn Glu Thr Tyr	Thr Lys Ile Val	Leu Leu Asp Phe	
	260	265	270	
cac cac tct ggg acc	tct gta aat tgc	atc gta gag gaa	gtg gat gca	864
His His Ser Gly	Thr Ser Val Asn	Cys Ile Val Glu	Glu Val Asp Ala	
	275	280	285	
aga tct gta tat cca	tat gac tca ttt	gct atc tcc act	ggg gac gtg	912
Arg Ser Val Tyr	Pro Tyr Asp Ser	Phe Ala Ile Ser	Thr Gly Asp Val	
	290	295	300	
att cac atg tct cca	ttc ttt ggg ctg	agg gat gga gcc	cat gta gaa	960
Ile His Met Ser	Pro Phe Phe Gly	Leu Arg Asp Gly	Ala His Val Glu	
	305	310	315	320
cat act agt tat tct	tca gac aga ttt	caa caa atc gag	gga tac tat	1008
His Thr Ser Tyr	Ser Ser Asp Arg	Phe Gln Gln Ile	Glu Gly Tyr Tyr	
	325	330	335	
cca ata gac ttg gat	acc gat tac act	ggg gca cca gtt	tct cgc aat	1056
Pro Ile Asp Leu	Asp Thr Asp Tyr	Thr Gly Ala Pro	Val Ser Arg Asn	
	340	345	350	
ttt ttg gaa act ccg	cat gtg aca gtg	gcc tgg aac tgg	acc cca aag	1104
Phe Leu Glu Thr	Pro His Val Thr	Val Ala Trp Asn	Trp Thr Pro Lys	
	355	360	365	
tct ggt cgg gta tgt	acc tta gcc aaa	tgg agg gaa ata	gat gaa atg	1152
Ser Gly Arg Val	Cys Thr Leu Ala	Lys Trp Arg Glu	Ile Asp Glu Met	
	370	375	380	
cta ccg atg aat ata	ggc tcc tat aga	ttt aca gcc aag	acc ata tcc	1200
Leu Pro Met Asn	Ile Gly Ser Tyr	Arg Phe Thr Ala	Lys Thr Ile Ser	
	385	390	395	400
gct act ttc atc tcc	aat act tca caa	ttt gaa atc aat	cgt atc cgt	1248
Ala Thr Phe Ile	Ser Asn Thr Ser	Gln Phe Glu Ile	Asn Arg Ile Arg	
	405	410	415	
ttg ggg gac tgt gcc	acc aag gag gca	gcc gaa gcc ata	gac cgg att	1296
Leu Gly Asp Cys	Ala Thr Lys Glu	Ala Ala Glu Ala	Ile Asp Arg Ile	
	420	425	430	
tat aag agt aaa tat	agt aaa act cat	att cag act gga	acc ctg gag	1344
Tyr Lys Ser Lys	Tyr Ser Lys Thr	His Ile Gln Thr	Gly Thr Leu Glu	
	435	440	445	
acc tac cta gcc cgt	ggg gga ttt cta	ata gct ttc cgt	ccc atg atc	1392
Thr Tyr Leu Ala	Arg Gly Phe Leu	Ile Ala Phe Arg	Pro Met Ile	
	450	455	460	

agc aac gaa cta gca aag tta tat atc aat gaa tta gca cgt tcc aat	1440
Ser Asn Glu Leu Ala Lys Leu Tyr Ile Asn Glu Leu Ala Arg Ser Asn	
465 470 475 480	
cgc acg gta gtg gat ctc agt gca ctc ctc aat cca tct ggg gaa aca	1488
Arg Thr Val Val Asp Leu Ser Ala Leu Leu Asn Pro Ser Gly Glu Thr	
485 490 495	
gta caa cga act aga aga tcg gtc cca tct aat caa cat cat agg tcg	1536
Val Gln Arg Thr Arg Arg Ser Val Pro Ser Asn Gln His His Arg Ser	
500 505 510	
cgg cgc agc aca ata gag ggg ggt ata gaa acc gtg aac aat gca tca	1584
Arg Arg Ser Thr Ile Glu Gly Gly Ile Glu Thr Val Asn Asn Ala Ser	
515 520 525	
ctc ctc aag acc acc tca tct gtg gaa ttc gca atg cta caa ttt gcc	1632
Leu Leu Lys Thr Thr Ser Ser Val Glu Phe Ala Met Leu Gln Phe Ala	
530 535 540	
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Tyr Asp Tyr Ile Gln Ala His Val Asn Glu Met Leu Ser Arg Ile Ala	
545 550 555 560	
act gcc tgg tgt aca ctt cag aac cgc gaa cat gtg ctg tgg aca gag	1728
Thr Ala Trp Cys Thr Leu Gln Asn Arg Glu His Val Leu Trp Thr Glu	
565 570 575	
acc cta aaa ctc aat ccc ggt ggg gtg gtc tcg atg gcc cta gaa cgt	1776
Thr Leu Lys Leu Asn Pro Gly Gly Val Val Ser Met Ala Leu Glu Arg	
580 585 590	
cgt gta tcc gcg cgc cta ctt gga gat gcc gtc gcc gta aca caa tgt	1824
Arg Val Ser Ala Arg Leu Leu Gly Asp Ala Val Ala Val Thr Gln Cys	
595 600 605	
gtt aac att tct agc gga cat gtc tat atc caa aat tct atg cgg gtg	1872
Val Asn Ile Ser Ser Gly His Val Tyr Ile Gln Asn Ser Met Arg Val	
610 615 620	
acg ggt tca tca acg aca tgt tac agc cgc cct ctt gtt tcc ttc cgt	1920
Thr Gly Ser Ser Thr Thr Cys Tyr Ser Arg Pro Leu Val Ser Phe Arg	
625 630 635 640	
gcc ctc aat gac tcc gaa tac ata gaa gga caa cta ggg gaa aac aat	1968
Ala Leu Asn Asp Ser Glu Tyr Ile Glu Gly Gln Leu Gly Glu Asn Asn	
645 650 655	
gaa ctt ctc gtg gaa cga aaa cta att gag cct tgc act gtc aat aat	2016
Glu Leu Leu Val Glu Arg Lys Leu Ile Glu Pro Cys Thr Val Asn Asn	
660 665 670	
aag cgg tat ttt aag ttt ggg gca gat tat gta tat ttt gag gat tat	2064
Lys Arg Tyr Phe Lys Phe Gly Ala Asp Tyr Val Tyr Phe Glu Asp Tyr	
675 680 685	

gcg tat gtc cgt aaa gtc ccg cta tgc gag ata gaa ctg ata agt gcg Ala Tyr Val Arg Lys Val Pro Leu Ser Glu Ile Glu Leu Ile Ser Ala 690 695 700	2112
tat gtg att aaa tct act ctc cta gag gat cgt gaa ttt ctc cac tca Tyr Val Ile Lys Ser Thr Leu Leu Glu Asp Arg Glu Phe Leu His Ser 705 710 715 720	2160
agt tat aca cga gct gag ctg gaa gat acc ggc cct ttt gac tac agc Ser Tyr Thr Arg Ala Glu Leu Glu Asp Thr Gly Pro Phe Asp Tyr Ser 725 730 735	2208
gag att caa cgc cgc aac caa ctc cac gcc tta aaa ttt tat gat ata Glu Ile Gln Arg Arg Asn Gln Leu His Ala Leu Lys Phe Tyr Asp Ile 740 745 750	2256
gac agc ata gtc aga gtg gat aat aat ctt gtc atc atg cgt ggt atg Asp Ser Ile Val Arg Val Asp Asn Asn Leu Val Ile Met Arg Gly Met 755 760 765	2304
gca aat ttt ttt cag gga ctc ggg gat gtg ggg gct ggt ttc ggc aag Ala Asn Phe Phe Gln Gly Leu Gly Asp Val Gly Ala Gly Phe Gly Lys 770 775 780	2352
gtg gtc tta ggg gct gcg agt gcg gta atc tca aca gta tca ggc gta Val Val Leu Gly Ala Ala Ser Ala Val Ile Ser Thr Val Ser Gly Val 785 790 795 800	2400
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ata tta gct ggc atc gtc gca gca ttc ctg gca tat cgc tat ata tct Ile Leu Ala Gly Ile Val Ala Ala Phe Leu Ala Tyr Arg Tyr Ile Ser 820 825 830	2496
aga tta cgt gca aat cca atg aaa gcc tta tat cct gtg acg act agg Arg Leu Arg Ala Asn Pro Met Lys Ala Leu Tyr Pro Val Thr Thr Arg 835 840 845	2544
aat ttg aaa cag acg gct aag agc ccc gcc tca acg gct ggt ggg gat Asn Leu Lys Gln Thr Ala Lys Ser Pro Ala Ser Thr Ala Gly Gly Asp 850 855 860	2592
agc gac ccg gga gtc gat gac ttc gat gag gaa aag cta atg cag gca Ser Asp Pro Gly Val Asp Asp Phe Asp Glu Glu Lys Leu Met Gln Ala 865 870 875 880	2640
agg gag atg ata aaa tat atg tcc ctc gta tgc gct atg gag caa caa Arg Glu Met Ile Lys Tyr Met Ser Leu Val Ser Ala Met Glu Gln Gln 885 890 895	2688
gaa cat aag gcg atg aaa aag aat aag ggc cca gcg atc cta acg agt Glu His Lys Ala Met Lys Lys Asn Lys Gly Pro Ala Ile Leu Thr Ser 900 905 910	2736
cat ctc act aac atg gcc ctc cgt cgc cgt gga cct aaa tac caa cgc	2784

His Leu Thr Asn Met Ala Leu Arg Arg Arg Gly Pro Lys Tyr Gln Arg
 915 920 925

ctc aat aat ctt gat agc ggt gat gat act gaa aca aat ctt gtc 2829
 Leu Asn Asn Leu Asp Ser Gly Asp Asp Thr Glu Thr Asn Leu Val
 930 935 940

<210> 14
 <211> 943
 <212> PRT
 <213> Feline herpesvirus 1

<400> 14
 Met Ser Thr Arg Gly Asp Leu Gly Lys Arg Arg Arg Gly Ser Arg Trp
 1 5 10 15
 Gln Gly His Ser Gly Tyr Phe Arg Gln Arg Cys Phe Phe Pro Ser Leu
 20 25 30
 Leu Gly Ile Ala Ala Thr Gly Ser Arg His Gly Asn Gly Ser Ser Gly
 35 40 45
 Leu Thr Arg Leu Ala Arg Tyr Val Ser Phe Ile Trp Ile Val Leu Phe
 50 55 60
 Leu Val Gly Pro Arg Pro Val Glu Gly Gln Ser Gly Ser Thr Ser Glu
 65 70 75 80
 Gln Pro Arg Arg Thr Val Ala Thr Pro Glu Val Gly Val His His Gln
 85 90 95
 Asn Gln Leu Gln Ile Pro Pro Ile Cys Arg Tyr Glu Glu Ala Leu Arg
 100 105 110
 Ala Ser Gln Ile Glu Ala Asn Gly Pro Ser Thr Phe Tyr Met Cys Pro
 115 120 125
 Pro Pro Ser Gly Ser Thr Val Val Arg Leu Glu Pro Pro Arg Ala Cys
 130 135 140
 Pro Asp Tyr Lys Leu Gly Lys Asn Phe Thr Glu Gly Ile Ala Val Ile
 145 150 155 160
 Phe Lys Glu Asn Ile Ala Pro Tyr Lys Phe Lys Ala Asn Ile Tyr Tyr
 165 170 175
 Lys Asn Ile Ile Met Thr Thr Val Trp Ser Gly Ser Ser Tyr Ala Val
 180 185 190
 Thr Thr Asn Arg Tyr Thr Asp Arg Val Pro Val Lys Val Gln Glu Ile
 195 200 205
 Thr Asp Leu Ile Asp Arg Arg Gly Met Cys Leu Ser Lys Ala Asp Tyr
 210 215 220
 Val Arg Asn Asn Tyr Gln Phe Thr Ala Phe Asp Arg Asp Glu Asp Pro

225		230		235		240
Arg Glu Leu Pro	Leu Lys Pro Pro Ser Ser	Thr Leu Ser Arg Val Arg				
	245		250		255	
Gly Trp His Thr	Asn Glu Thr Tyr Thr Lys Ile Val Leu Leu Asp Phe					
	260		265		270	
His His Ser Gly Thr	Ser Val Asn Cys Ile Val Glu Glu Val Asp Ala					
	275		280		285	
Arg Ser Val Tyr Pro Tyr	Asp Ser Phe Ala Ile Ser Thr Gly Asp Val					
	290		295		300	
Ile His Met Ser Pro Phe	Phe Gly Leu Arg Asp Gly Ala His Val Glu					
305		310		315		320
His Thr Ser Tyr Ser Ser	Asp Arg Phe Gln Gln Ile Glu Gly Tyr Tyr					
	325		330		335	
Pro Ile Asp Leu Asp Thr	Asp Tyr Thr Gly Ala Pro Val Ser Arg Asn					
	340		345		350	
Phe Leu Glu Thr Pro His	Val Thr Val Ala Trp Asn Trp Thr Pro Lys					
	355		360		365	
Ser Gly Arg Val Cys Thr	Leu Ala Lys Trp Arg Glu Ile Asp Glu Met					
	370		375		380	
Leu Pro Met Asn Ile Gly	Ser Tyr Arg Phe Thr Ala Lys Thr Ile Ser					
385		390		395		400
Ala Thr Phe Ile Ser Asn	Thr Ser Gln Phe Glu Ile Asn Arg Ile Arg					
	405		410		415	
Leu Gly Asp Cys Ala Thr	Lys Glu Ala Ala Glu Ala Ile Asp Arg Ile					
	420		425		430	
Tyr Lys Ser Lys Tyr Ser	Lys Thr His Ile Gln Thr Gly Thr Leu Glu					
	435		440		445	
Thr Tyr Leu Ala Arg Gly	Gly Phe Leu Ile Ala Phe Arg Pro Met Ile					
	450		455		460	
Ser Asn Glu Leu Ala Lys	Leu Tyr Ile Asn Glu Leu Ala Arg Ser Asn					
465		470		475		480
Arg Thr Val Val Asp	Leu Ser Ala Leu Leu Asn Pro Ser Gly Glu Thr					
	485		490		495	
Val Gln Arg Thr Arg	Arg Ser Val Pro Ser Asn Gln His His Arg Ser					
	500		505		510	
Arg Arg Ser Thr Ile	Glu Gly Gly Ile Glu Thr Val Asn Asn Ala Ser					
	515		520		525	
Leu Leu Lys Thr Thr	Ser Ser Val Glu Phe Ala Met Leu Gln Phe Ala					

835	840	845	
Asn Leu Lys Gln Thr Ala Lys Ser Pro Ala Ser Thr Ala Gly Gly Asp			
850	855	860	
Ser Asp Pro Gly Val Asp Asp Phe Asp Glu Glu Lys Leu Met Gln Ala			
865	870	875	880
Arg Glu Met Ile Lys Tyr Met Ser Leu Val Ser Ala Met Glu Gln Gln			
	885	890	895
Glu His Lys Ala Met Lys Lys Asn Lys Gly Pro Ala Ile Leu Thr Ser			
	900	905	910
His Leu Thr Asn Met Ala Leu Arg Arg Arg Gly Pro Lys Tyr Gln Arg			
	915	920	925
Leu Asn Asn Leu Asp Ser Gly Asp Asp Thr Glu Thr Asn Leu Val			
930	935	940	
<210> 15			
<211> 750			
<212> DNA			
<213> Feline herpesvirus 1			
<220>			
<221> CDS			
<222> (1)..(750)			
<400> 15			
atg tcc act cgt ggc gat ctt ggg aag cgg cga cga ggg agt cgt tgg			48
Met Ser Thr Arg Gly Asp Leu Gly Lys Arg Arg Arg Gly Ser Arg Trp			
1	5	10	15
cag gga cac agt ggc tat ttt cga cag aga tgt ttt ttc cct tct cta			96
Gln Gly His Ser Gly Tyr Phe Arg Gln Arg Cys Phe Phe Pro Ser Leu			
	20	25	30
ctc ggt att gca gcg act ggc tcc aga cat ggt aac gga tcg tcg gga			144
Leu Gly Ile Ala Ala Thr Gly Ser Arg His Gly Asn Gly Ser Ser Gly			
	35	40	45
tta acc aga cta gct aga tat gtt tca ttt atc tgg atc gta cta ttc			192
Leu Thr Arg Leu Ala Arg Tyr Val Ser Phe Ile Trp Ile Val Leu Phe			
	50	55	60
tta gtc ggt ccc cgt cca gta gag ggt caa tct gga agc aca tcg gaa			240
Leu Val Gly Pro Arg Pro Val Glu Gly Gln Ser Gly Ser Thr Ser Glu			
65	70	75	80
caa ccc cgg cgg act gta gct acc cct gag gta ggg gta cac cac caa			288
Gln Pro Arg Arg Thr Val Ala Thr Pro Glu Val Gly Val His His Gln			
	85	90	95
aac caa cta cag atc cca ccg ata tgt cga tat gag gaa gct ctc cgt			336

Asn	Gln	Leu	Gln	Ile	Pro	Pro	Ile	Cys	Arg	Tyr	Glu	Glu	Ala	Leu	Arg		
			100					105					110				
gcg	tcc	caa	ata	gag	gct	aac	gga	cca	tcg	act	ttt	tat	atg	tgt	cca	384	
Ala	Ser	Gln	Ile	Glu	Ala	Asn	Gly	Pro	Ser	Thr	Phe	Tyr	Met	Cys	Pro		
		115					120					125					
cca	cct	tca	gga	tct	act	gtc	gtg	cgt	tta	gag	cca	cca	cgg	gcc	tgt	432	
Pro	Pro	Ser	Gly	Ser	Thr	Val	Val	Arg	Leu	Glu	Pro	Pro	Arg	Ala	Cys		
		130				135					140						
cca	gat	tat	aaa	cta	ggg	aaa	aat	ttt	acc	gag	ggt	ata	gct	gta	ata	480	
Pro	Asp	Tyr	Lys	Leu	Gly	Lys	Asn	Phe	Thr	Glu	Gly	Ile	Ala	Val	Ile		
145					150					155					160		
ttt	aaa	gaa	aat	ata	gcg	cca	tat	aaa	ttc	aag	gca	aat	ata	tac	tat	528	
Phe	Lys	Glu	Asn	Ile	Ala	Pro	Tyr	Lys	Phe	Lys	Ala	Asn	Ile	Tyr	Tyr		
				165				170						175			
aaa	aac	att	att	atg	aca	acg	gta	tgg	tct	ggg	agt	tcc	tat	gcc	ggt	576	
Lys	Asn	Ile	Ile	Met	Thr	Thr	Val	Trp	Ser	Gly	Ser	Ser	Tyr	Ala	Val		
			180					185					190				
aca	acc	aac	cga	tat	aca	gac	agg	ggt	ccc	gtg	aaa	ggt	caa	gag	att	624	
Thr	Thr	Asn	Arg	Tyr	Thr	Asp	Arg	Val	Pro	Val	Lys	Val	Gln	Glu	Ile		
		195					200					205					
aca	gat	ctc	ata	gat	aga	cgg	ggt	atg	tgc	ctc	tcg	aaa	gct	gat	tac	672	
Thr	Asp	Leu	Ile	Asp	Arg	Arg	Gly	Met	Cys	Leu	Ser	Lys	Ala	Asp	Tyr		
		210				215					220						
ggt	cgt	aac	aat	tat	caa	ttt	acg	gcc	ttt	gat	cga	gac	gag	gat	ccc	720	
Val	Arg	Asn	Asn	Tyr	Gln	Phe	Thr	Ala	Phe	Asp	Arg	Asp	Glu	Asp	Pro		
225					230				235						240		
aga	gaa	ctg	cct	ctg	aaa	cct	cca	agt	tca							750	
Arg	Glu	Leu	Pro	Leu	Lys	Pro	Pro	Ser	Ser								
				245				250									

<210> 16
 <211> 250
 <212> PRT
 <213> Feline herpesvirus 1

<400> 16
 Met Ser Thr Arg Gly Asp Leu Gly Lys Arg Arg Arg Gly Ser Arg Trp
 1 5 10 15
 Gln Gly His Ser Gly Tyr Phe Arg Gln Arg Cys Phe Phe Pro Ser Leu
 20 25 30
 Leu Gly Ile Ala Ala Thr Gly Ser Arg His Gly Asn Gly Ser Ser Gly
 35 40 45
 Leu Thr Arg Leu Ala Arg Tyr Val Ser Phe Ile Trp Ile Val Leu Phe
 50 55 60

Leu Val Gly Pro Arg Pro Val Glu Gly Gln Ser Gly Ser Thr Ser Glu
 65 70 75 80
 Gln Pro Arg Arg Thr Val Ala Thr Pro Glu Val Gly Val His His Gln
 85 90 95
 Asn Gln Leu Gln Ile Pro Pro Ile Cys Arg Tyr Glu Glu Ala Leu Arg
 100 105 110
 Ala Ser Gln Ile Glu Ala Asn Gly Pro Ser Thr Phe Tyr Met Cys Pro
 115 120 125
 Pro Pro Ser Gly Ser Thr Val Val Arg Leu Glu Pro Pro Arg Ala Cys
 130 135 140
 Pro Asp Tyr Lys Leu Gly Lys Asn Phe Thr Glu Gly Ile Ala Val Ile
 145 150 155 160
 Phe Lys Glu Asn Ile Ala Pro Tyr Lys Phe Lys Ala Asn Ile Tyr Tyr
 165 170 175
 Lys Asn Ile Ile Met Thr Thr Val Trp Ser Gly Ser Ser Tyr Ala Val
 180 185 190
 Thr Thr Asn Arg Tyr Thr Asp Arg Val Pro Val Lys Val Gln Glu Ile
 195 200 205
 Thr Asp Leu Ile Asp Arg Arg Gly Met Cys Leu Ser Lys Ala Asp Tyr
 210 215 220
 Val Arg Asn Asn Tyr Gln Phe Thr Ala Phe Asp Arg Asp Glu Asp Pro
 225 230 235 240
 Arg Glu Leu Pro Leu Lys Pro Pro Ser Ser
 245 250

<210> 17
 <211> 1602
 <212> DNA
 <213> Feline herpesvirus 1

<220>
 <221> CDS
 <222> (1)..(1602)

<400> 17
 atg aga cga tat agg atg gga cgc gga atc tac ctt ctc tat atc tgt 48
 Met Arg Arg Tyr Arg Met Gly Arg Gly Ile Tyr Leu Leu Tyr Ile Cys
 1 5 10 15
 ctg tta tat aca tat ctc cag ttt ggt act tcg tcg aca acc gcg gtc 96
 Leu Leu Tyr Thr Tyr Leu Gln Phe Gly Thr Ser Ser Thr Thr Ala Val
 20 25 30

agc atg tcc gct acc acc ccg ata tcc cag cca aca tct cca ttc act	192
Ser Met Ser Ser Ala Thr Thr Pro Ile Ser Gln Pro Thr Ser Pro Phe Thr	
50 55 60	
act cca act aga aga tct aca aat ata gct aca agt tcg agt acc acc	240
Thr Pro Thr Arg Arg Ser Thr Asn Ile Ala Thr Ser Ser Ser Thr Thr	
65 70 75 80	
cag gca tcc cag cca aca tct aca tta act act cta act aga agc tcg	288
Gln Ala Ser Gln Pro Thr Ser Thr Leu Thr Thr Leu Thr Arg Ser Ser	
85 90 95	
aca act ata gct aca agt ccg agt acc acc cag gca gcc aca ttc ata	336
Thr Thr Ile Ala Thr Ser Pro Ser Thr Thr Gln Ala Ala Thr Phe Ile	
100 105 110	
gga tca tct acc gat tcc aat acc act tta ctc aaa aca aca aaa aaa	384
Gly Ser Ser Thr Asp Ser Asn Thr Thr Leu Leu Lys Thr Thr Lys Lys	
115 120 125	
cca aag cgt aaa aag aat aag aat aac ggg gcc aga ttt aaa tta tat	432
Pro Lys Arg Lys Lys Asn Lys Asn Asn Gly Ala Arg Phe Lys Leu Tyr	
130 135 140	
tgt gga tat aag ggg gtt atc tac aga ccg tat ttt agc cct ctt cag	480
Cys Gly Tyr Lys Gly Val Ile Tyr Arg Pro Tyr Phe Ser Pro Leu Gln	
145 150 155 160	
cta aac tgt act cta ccc aca gaa cct cat att acc aac cct att gac	528
Leu Asn Cys Thr Leu Pro Thr Glu Pro His Ile Thr Asn Pro Ile Asp	
165 170 175	
ttc gag atc tgg ttt aaa cca cgc acc aga ttt ggg gat ttt ctt ggg	576
Phe Glu Ile Trp Phe Lys Pro Arg Thr Arg Phe Gly Asp Phe Leu Gly	
180 185 190	
gat aaa gaa gac ttc gta ggg aat cat acc cgc acc agc ata tta cta	624
Asp Lys Glu Asp Phe Val Gly Asn His Thr Arg Thr Ser Ile Leu Leu	
195 200 205	
ttt agc agc cgt aat ggg agt gtt aat tcc atg gat ctt ggg gac gcg	672
Phe Ser Ser Arg Asn Gly Ser Val Asn Ser Met Asp Leu Gly Asp Ala	
210 215 220	
aca ctc ggg atc cta caa tct agg ata cca gat tac aca tta tat aat	720
Thr Leu Gly Ile Leu Gln Ser Arg Ile Pro Asp Tyr Thr Leu Tyr Asn	
225 230 235 240	
att ccc ata caa cat acc gaa gcg atg tca ttg gga atc aaa tct gtg	768
Ile Pro Ile Gln His Thr Glu Ala Met Ser Leu Gly Ile Lys Ser Val	
245 250 255	
gaa tct gcc acg tcc ggt gtt tat aca tgg cgg gtc tat ggt gga gat	816

Glu	Ser	Ala	Thr	Ser	Gly	Val	Tyr	Thr	Trp	Arg	Val	Tyr	Gly	Gly	Asp	
			260					265					270			
gta	cta	aat	aaa	aca	gtg	cta	gga	cag	gta	aat	gta	tct	gta	gtg	gca	864
Val	Leu	Asn	Lys	Thr	Val	Leu	Gly	Gln	Val	Asn	Val	Ser	Val	Val	Ala	
		275					280					285				
tat	cac	ccc	ccg	agc	gta	aat	ctt	aca	cca	cgc	gcc	agt	cta	ttt	aat	912
Tyr	His	Pro	Pro	Ser	Val	Asn	Leu	Thr	Pro	Arg	Ala	Ser	Leu	Phe	Asn	
	290					295					300					
aag	acc	ttt	gag	gcg	gta	tgt	gca	gtg	gcg	aat	tac	ttc	ccc	ccg	cga	960
Lys	Thr	Phe	Glu	Ala	Val	Cys	Ala	Val	Ala	Asn	Tyr	Phe	Pro	Pro	Arg	
305					310					315					320	
tcc	acg	aaa	cta	aca	tgg	tat	ctt	gac	ggg	aag	cca	ata	gaa	agg	caa	1008
Ser	Thr	Lys	Leu	Thr	Trp	Tyr	Leu	Asp	Gly	Lys	Pro	Ile	Glu	Arg	Gln	
				325					330					335		
tac	att	tca	gat	acg	gca	agt	gta	tgg	ata	gat	gga	ctc	atc	acc	aga	1056
Tyr	Ile	Ser	Asp	Thr	Ala	Ser	Val	Trp	Ile	Asp	Gly	Leu	Ile	Thr	Arg	
			340					345					350			
agt	tct	gtg	ttg	gct	att	ccg	aca	act	gaa	aca	gat	tcc	gag	aaa	cca	1104
Ser	Ser	Val	Leu	Ala	Ile	Pro	Thr	Thr	Glu	Thr	Asp	Ser	Glu	Lys	Pro	
		355					360					365				
gat	ata	cga	tgt	gat	ttg	gaa	tgg	cat	gaa	agt	cct	gtg	tcc	tat	aag	1152
Asp	Ile	Arg	Cys	Asp	Leu	Glu	Trp	His	Glu	Ser	Pro	Val	Ser	Tyr	Lys	
	370					375					380					
aga	ttc	acg	aaa	agt	gta	gcc	ccg	gac	gtc	tat	tac	cca	cct	act	gtg	1200
Arg	Phe	Thr	Lys	Ser	Val	Ala	Pro	Asp	Val	Tyr	Tyr	Pro	Pro	Thr	Val	
385					390					395					400	
tct	gtt	acc	ttc	gct	gat	aca	cgg	gct	ata	tgt	gat	gtt	aaa	tgt	gta	1248
Ser	Val	Thr	Phe	Ala	Asp	Thr	Arg	Ala	Ile	Cys	Asp	Val	Lys	Cys	Val	
				405					410					415		
cca	cgg	gac	ggg	ata	tcc	ttg	atg	tgg	aaa	att	ggg	aac	tac	cat	cta	1296
Pro	Arg	Asp	Gly	Ile	Ser	Leu	Met	Trp	Lys	Ile	Gly	Asn	Tyr	His	Leu	
			420					425					430			
cca	aaa	gca	atg	agt	gct	gat	ata	ctg	atc	aca	ggg	ccg	tgt	ata	gaa	1344
Pro	Lys	Ala	Met	Ser	Ala	Asp	Ile	Leu	Ile	Thr	Gly	Pro	Cys	Ile	Glu	
		435				440						445				
cgt	cca	ggg	ttg	gtc	aac	att	cag	agt	atg	tgt	gat	ata	tca	gaa	acg	1392
Arg	Pro	Gly	Leu	Val	Asn	Ile	Gln	Ser	Met	Cys	Asp	Ile	Ser	Glu	Thr	
	450					455					460					
gat	gga	ccc	gtg	agt	tat	acc	tgt	cag	acc	atc	gga	tac	cca	cca	att	1440
Asp	Gly	Pro	Val	Ser	Tyr	Thr	Cys	Gln	Thr	Ile	Gly	Tyr	Pro	Pro	Ile	
465					470					475					480	
cta	ccg	gga	ttt	tac	gac	aca	caa	gtc	tac	gac	gcg	tcc	cct	gaa	atc	1488
Leu	Pro	Gly	Phe	Tyr	Asp	Thr	Gln	Val	Tyr	Asp	Ala	Ser	Pro	Glu	Ile	

485	490	495	
gtc agt gaa tca atg ttg gtt agt gtc gtt gct gta ata cta gga gct			1536
Val Ser Glu Ser Met Leu Val Ser Val Val Ala Val Ile Leu Gly Ala			
500	505	510	
gtt ctc atc aca gtc ttt atc ttt att acg gca tta tgt tta tat tat			1584
Val Leu Ile Thr Val Phe Ile Phe Ile Thr Ala Leu Cys Leu Tyr Tyr			
515	520	525	
tct cat ccc cgg cga tta			1602
Ser His Pro Arg Arg Leu			
530			
<210> 18			
<211> 534			
<212> PRT			
<213> Feline herpesvirus 1			
<400> 18			
Met Arg Arg Tyr Arg Met Gly Arg Gly Ile Tyr Leu Leu Tyr Ile Cys			
1	5	10	15
Leu Leu Tyr Thr Tyr Leu Gln Phe Gly Thr Ser Ser Thr Thr Ala Val			
20	25	30	
Ser Ile Glu Asn Ser Asp Asn Ser Thr Ala Glu Met Leu Ser Ser Thr			
35	40	45	
Ser Met Ser Ala Thr Thr Pro Ile Ser Gln Pro Thr Ser Pro Phe Thr			
50	55	60	
Thr Pro Thr Arg Arg Ser Thr Asn Ile Ala Thr Ser Ser Ser Thr Thr			
65	70	75	80
Gln Ala Ser Gln Pro Thr Ser Thr Leu Thr Thr Leu Thr Arg Ser Ser			
85	90	95	
Thr Thr Ile Ala Thr Ser Pro Ser Thr Thr Gln Ala Ala Thr Phe Ile			
100	105	110	
Gly Ser Ser Thr Asp Ser Asn Thr Thr Leu Leu Lys Thr Thr Lys Lys			
115	120	125	
Pro Lys Arg Lys Lys Asn Lys Asn Asn Gly Ala Arg Phe Lys Leu Tyr			
130	135	140	
Cys Gly Tyr Lys Gly Val Ile Tyr Arg Pro Tyr Phe Ser Pro Leu Gln			
145	150	155	160
Leu Asn Cys Thr Leu Pro Thr Glu Pro His Ile Thr Asn Pro Ile Asp			
165	170	175	
Phe Glu Ile Trp Phe Lys Pro Arg Thr Arg Phe Gly Asp Phe Leu Gly			
180	185	190	

Asp Lys Glu Asp Phe Val Gly Asn His Thr Arg Thr Ser Ile Leu Leu
 195 200 205
 Phe Ser Ser Arg Asn Gly Ser Val Asn Ser Met Asp Leu Gly Asp Ala
 210 215 220
 Thr Leu Gly Ile Leu Gln Ser Arg Ile Pro Asp Tyr Thr Leu Tyr Asn
 225 230 235 240
 Ile Pro Ile Gln His Thr Glu Ala Met Ser Leu Gly Ile Lys Ser Val
 245 250 255
 Glu Ser Ala Thr Ser Gly Val Tyr Thr Trp Arg Val Tyr Gly Gly Asp
 260 265 270
 Val Leu Asn Lys Thr Val Leu Gly Gln Val Asn Val Ser Val Val Ala
 275 280 285
 Tyr His Pro Pro Ser Val Asn Leu Thr Pro Arg Ala Ser Leu Phe Asn
 290 295 300
 Lys Thr Phe Glu Ala Val Cys Ala Val Ala Asn Tyr Phe Pro Pro Arg
 305 310 315 320
 Ser Thr Lys Leu Thr Trp Tyr Leu Asp Gly Lys Pro Ile Glu Arg Gln
 325 330 335
 Tyr Ile Ser Asp Thr Ala Ser Val Trp Ile Asp Gly Leu Ile Thr Arg
 340 345 350
 Ser Ser Val Leu Ala Ile Pro Thr Thr Glu Thr Asp Ser Glu Lys Pro
 355 360 365
 Asp Ile Arg Cys Asp Leu Glu Trp His Glu Ser Pro Val Ser Tyr Lys
 370 375 380
 Arg Phe Thr Lys Ser Val Ala Pro Asp Val Tyr Tyr Pro Pro Thr Val
 385 390 395 400
 Ser Val Thr Phe Ala Asp Thr Arg Ala Ile Cys Asp Val Lys Cys Val
 405 410 415
 Pro Arg Asp Gly Ile Ser Leu Met Trp Lys Ile Gly Asn Tyr His Leu
 420 425 430
 Pro Lys Ala Met Ser Ala Asp Ile Leu Ile Thr Gly Pro Cys Ile Glu
 435 440 445
 Arg Pro Gly Leu Val Asn Ile Gln Ser Met Cys Asp Ile Ser Glu Thr
 450 455 460
 Asp Gly Pro Val Ser Tyr Thr Cys Gln Thr Ile Gly Tyr Pro Pro Ile
 465 470 475 480
 Leu Pro Gly Phe Tyr Asp Thr Gln Val Tyr Asp Ala Ser Pro Glu Ile
 485 490 495

Val Ser Glu Ser Met Leu Val Ser Val Val Ala Val Ile Leu Gly Ala
500 505 510

Val Leu Ile Thr Val Phe Ile Phe Ile Thr Ala Leu Cys Leu Tyr Tyr
515 520 525

Ser His Pro Arg Arg Leu
530

<210> 19

<211> 1401

<212> DNA

<213> Feline herpesvirus 1

<220>

<221> CDS

<222> (1)..(1401)

<400> 19

agt att gaa aat agt gat aat agt act gcg gag atg tta tca tct acc	48
Ser Ile Glu Asn Ser Asp Asn Ser Thr Ala Glu Met Leu Ser Ser Thr	
1 5 10 15	
agc atg tcc gct acc acc ccg ata tcc cag cca aca tct cca ttc act	96
Ser Met Ser Ala Thr Thr Pro Ile Ser Gln Pro Thr Ser Pro Phe Thr	
20 25 30	
act cca act aga aga tct aca aat ata gct aca agt tcg agt acc acc	144
Thr Pro Thr Arg Arg Ser Thr Asn Ile Ala Thr Ser Ser Ser Thr Thr	
35 40 45	
cag gca tcc cag cca aca tct aca tta act act cta act aga agc tcg	192
Gln Ala Ser Gln Pro Thr Ser Thr Leu Thr Thr Leu Thr Arg Ser Ser	
50 55 60	
aca act ata gct aca agt ccg agt acc acc cag gca gcc aca ttc ata	240
Thr Thr Ile Ala Thr Ser Pro Ser Thr Thr Gln Ala Ala Thr Phe Ile	
65 70 75 80	
gga tca tct acc gat tcc aat acc act tta ctc aaa aca aca aaa aaa	288
Gly Ser Ser Thr Asp Ser Asn Thr Thr Leu Leu Lys Thr Thr Lys Lys	
85 90 95	
cca aag cgt aaa aag aat aag aat aac ggg gcc aga ttt aaa tta tat	336
Pro Lys Arg Lys Lys Asn Lys Asn Asn Gly Ala Arg Phe Lys Leu Tyr	
100 105 110	
tgt gga tat aag ggg gtt atc tac aga ccg tat ttt agc cct ctt cag	384
Cys Gly Tyr Lys Gly Val Ile Tyr Arg Pro Tyr Phe Ser Pro Leu Gln	
115 120 125	
cta aac tgt act cta ccc aca gaa cct cat att acc aac cct att gac	432
Leu Asn Cys Thr Leu Pro Thr Glu Pro His Ile Thr Asn Pro Ile Asp	
130 135 140	

ttc gag atc tgg ttt aaa cca cgc acc aga ttt ggg gat ttt ctt ggg	480
Phe Glu Ile Trp Phe Lys Pro Arg Thr Arg Phe Gly Asp Phe Leu Gly	
145 150 155 160	
gat aaa gaa gac ttc gta ggg aat cat acc cgc acc agc ata tta cta	528
Asp Lys Glu Asp Phe Val Gly Asn His Thr Arg Thr Ser Ile Leu Leu	
165 170 175	
ttt agc agc cgt aat ggg agt gtt aat tcc atg gat ctt ggg gac gcg	576
Phe Ser Ser Arg Asn Gly Ser Val Asn Ser Met Asp Leu Gly Asp Ala	
180 185 190	
aca ctc ggg atc cta caa tct agg ata cca gat tac aca tta tat aat	624
Thr Leu Gly Ile Leu Gln Ser Arg Ile Pro Asp Tyr Thr Leu Tyr Asn	
195 200 205	
att ccc ata caa cat acc gaa gcg atg tca ttg gga atc aaa tct gtg	672
Ile Pro Ile Gln His Thr Glu Ala Met Ser Leu Gly Ile Lys Ser Val	
210 215 220	
gaa tct gcc acg tcc ggt gtt tat aca tgg cgg gtc tat ggt gga gat	720
Glu Ser Ala Thr Ser Gly Val Tyr Thr Trp Arg Val Tyr Gly Gly Asp	
225 230 235 240	
gta cta aat aaa aca gtg cta gga cag gta aat gta tct gta gtg gca	768
Val Leu Asn Lys Thr Val Leu Gly Gln Val Asn Val Ser Val Val Ala	
245 250 255	
tat cac ccc ccg agc gta aat ctt aca cca cgc gcc agt cta ttt aat	816
Tyr His Pro Pro Ser Val Asn Leu Thr Pro Arg Ala Ser Leu Phe Asn	
260 265 270	
aag acc ttt gag gcg gta tgt gca gtg gcg aat tac ttc ccc ccg cga	864
Lys Thr Phe Glu Ala Val Cys Ala Val Ala Asn Tyr Phe Pro Pro Arg	
275 280 285	
tcc acg aaa cta aca tgg tat ctt gac ggg aag cca ata gaa agg caa	912
Ser Thr Lys Leu Thr Trp Tyr Leu Asp Gly Lys Pro Ile Glu Arg Gln	
290 295 300	
tac att tca gat acg gca agt gta tgg ata gat gga ctc atc acc aga	960
Tyr Ile Ser Asp Thr Ala Ser Val Trp Ile Asp Gly Leu Ile Thr Arg	
305 310 315 320	
agt tct gtg ttg gct att ccg aca act gaa aca gat tcc gag aaa cca	1008
Ser Ser Val Leu Ala Ile Pro Thr Thr Glu Thr Asp Ser Glu Lys Pro	
325 330 335	
gat ata cga tgt gat ttg gaa tgg cat gaa agt cct gtg tcc tat aag	1056
Asp Ile Arg Cys Asp Leu Glu Trp His Glu Ser Pro Val Ser Tyr Lys	
340 345 350	
aga ttc acg aaa agt gta gcc ccg gac gtc tat tac cca cct act gtg	1104
Arg Phe Thr Lys Ser Val Ala Pro Asp Val Tyr Tyr Pro Pro Thr Val	
355 360 365	
tct gtt acc ttc gct gat aca cgg gct ata tgt gat gtt aaa tgt gta	1152

Ser Val Thr Phe Ala Asp Thr Arg Ala Ile Cys Asp Val Lys Cys Val
 370 375 380

cca cgg gac ggg ata tcc ttg atg tgg aaa att ggt aac tac cat cta 1200
 Pro Arg Asp Gly Ile Ser Leu Met Trp Lys Ile Gly Asn Tyr His Leu
 385 390 395 400

cca aaa gca atg agt gct gat ata ctg atc aca ggt ccg tgt ata gaa 1248
 Pro Lys Ala Met Ser Ala Asp Ile Leu Ile Thr Gly Pro Cys Ile Glu
 405 410 415

cgt cca ggt ttg gtc aac att cag agt atg tgt gat ata tca gaa acg 1296
 Arg Pro Gly Leu Val Asn Ile Gln Ser Met Cys Asp Ile Ser Glu Thr
 420 425 430

gat gga ccc gtg agt tat acc tgt cag acc atc gga tac cca cca att 1344
 Asp Gly Pro Val Ser Tyr Thr Cys Gln Thr Ile Gly Tyr Pro Pro Ile
 435 440 445

cta ccg gga ttt tac gac aca caa gtc tac gac gcg tcc cct gaa atc 1392
 Leu Pro Gly Phe Tyr Asp Thr Gln Val Tyr Asp Ala Ser Pro Glu Ile
 450 455 460

gtc agt gaa 1401
 Val Ser Glu
 465

<210> 20
 <211> 467
 <212> PRT
 <213> Feline herpesvirus 1

<400> 20
 Ser Ile Glu Asn Ser Asp Asn Ser Thr Ala Glu Met Leu Ser Ser Thr
 1 5 10 15

Ser Met Ser Ala Thr Thr Pro Ile Ser Gln Pro Thr Ser Pro Phe Thr
 20 25 30

Thr Pro Thr Arg Arg Ser Thr Asn Ile Ala Thr Ser Ser Ser Thr Thr
 35 40 45

Gln Ala Ser Gln Pro Thr Ser Thr Leu Thr Thr Leu Thr Arg Ser Ser
 50 55 60

Thr Thr Ile Ala Thr Ser Pro Ser Thr Thr Gln Ala Ala Thr Phe Ile
 65 70 75 80

Gly Ser Ser Thr Asp Ser Asn Thr Thr Leu Leu Lys Thr Thr Lys Lys
 85 90 95

Pro Lys Arg Lys Lys Asn Lys Asn Asn Gly Ala Arg Phe Lys Leu Tyr
 100 105 110

Cys Gly Tyr Lys Gly Val Ile Tyr Arg Pro Tyr Phe Ser Pro Leu Gln
 115 120 125

Leu Asn Cys Thr Leu Pro Thr Glu Pro His Ile Thr Asn Pro Ile Asp
 130 135 140
 Phe Glu Ile Trp Phe Lys Pro Arg Thr Arg Phe Gly Asp Phe Leu Gly
 145 150 155 160
 Asp Lys Glu Asp Phe Val Gly Asn His Thr Arg Thr Ser Ile Leu Leu
 165 170 175
 Phe Ser Ser Arg Asn Gly Ser Val Asn Ser Met Asp Leu Gly Asp Ala
 180 185 190
 Thr Leu Gly Ile Leu Gln Ser Arg Ile Pro Asp Tyr Thr Leu Tyr Asn
 195 200 205
 Ile Pro Ile Gln His Thr Glu Ala Met Ser Leu Gly Ile Lys Ser Val
 210 215 220
 Glu Ser Ala Thr Ser Gly Val Tyr Thr Trp Arg Val Tyr Gly Gly Asp
 225 230 235 240
 Val Leu Asn Lys Thr Val Leu Gly Gln Val Asn Val Ser Val Val Ala
 245 250 255
 Tyr His Pro Pro Ser Val Asn Leu Thr Pro Arg Ala Ser Leu Phe Asn
 260 265 270
 Lys Thr Phe Glu Ala Val Cys Ala Val Ala Asn Tyr Phe Pro Pro Arg
 275 280 285
 Ser Thr Lys Leu Thr Trp Tyr Leu Asp Gly Lys Pro Ile Glu Arg Gln
 290 295 300
 Tyr Ile Ser Asp Thr Ala Ser Val Trp Ile Asp Gly Leu Ile Thr Arg
 305 310 315 320
 Ser Ser Val Leu Ala Ile Pro Thr Thr Glu Thr Asp Ser Glu Lys Pro
 325 330 335
 Asp Ile Arg Cys Asp Leu Glu Trp His Glu Ser Pro Val Ser Tyr Lys
 340 345 350
 Arg Phe Thr Lys Ser Val Ala Pro Asp Val Tyr Tyr Pro Pro Thr Val
 355 360 365
 Ser Val Thr Phe Ala Asp Thr Arg Ala Ile Cys Asp Val Lys Cys Val
 370 375 380
 Pro Arg Asp Gly Ile Ser Leu Met Trp Lys Ile Gly Asn Tyr His Leu
 385 390 395 400
 Pro Lys Ala Met Ser Ala Asp Ile Leu Ile Thr Gly Pro Cys Ile Glu
 405 410 415
 Arg Pro Gly Leu Val Asn Ile Gln Ser Met Cys Asp Ile Ser Glu Thr
 420 425 430

Asp Gly Pro Val Ser Tyr Thr Cys Gln Thr Ile Gly Tyr Pro Pro Ile
 435 440 445

Leu Pro Gly Phe Tyr Asp Thr Gln Val Tyr Asp Ala Ser Pro Glu Ile
 450 455 460

Val Ser Glu
 465

<210> 21
 <211> 1401
 <212> DNA
 <213> Feline herpesvirus 1

<220>
 <221> CDS
 <222> (1)..(1401)

<400> 21
 atg tcc atc gaa aac agc gat aat agt act gcg gag atg tta tca tct 48
 Met Ser Ile Glu Asn Ser Asp Asn Ser Thr Ala Glu Met Leu Ser Ser
 1 5 10 15
 acc agc atg tcc gct acc acc ccg ata tcc cag cca aca tct cca ttc 96
 Thr Ser Met Ser Ala Thr Thr Pro Ile Ser Gln Pro Thr Ser Pro Phe
 20 25 30
 act act cca act cgt cgc tct aca aat ata gct aca tcc tct tcc acc 144
 Thr Thr Pro Thr Arg Arg Ser Thr Asn Ile Ala Thr Ser Ser Ser Thr
 35 40 45
 acc cag gca tcc cag cca aca tct aca tta act act cta act aga agc 192
 Thr Gln Ala Ser Gln Pro Thr Ser Thr Leu Thr Thr Leu Thr Arg Ser
 50 55 60
 tcg aca act ata gct aca agt ccg agt acc acc cag gca gcc aca ttc 240
 Ser Thr Thr Ile Ala Thr Ser Pro Ser Thr Thr Gln Ala Ala Thr Phe
 65 70 75 80
 ata gga tca tct acc gat tcc aat acc act tta ctc aaa aca aca aaa 288
 Ile Gly Ser Ser Thr Asp Ser Asn Thr Thr Leu Leu Lys Thr Thr Lys
 85 90 95
 aaa cca aag cgt aaa aag aat aag aat aac ggg gcc aga ttt aaa tta 336
 Lys Pro Lys Arg Lys Lys Asn Lys Asn Asn Gly Ala Arg Phe Lys Leu
 100 105 110
 gat tgt gga tat aag ggg gtt atc tac aga ccg tat ttt agc cct ctt 384
 Asp Cys Gly Tyr Lys Gly Val Ile Tyr Arg Pro Tyr Phe Ser Pro Leu
 115 120 125
 cag cta aac tgt act cta ccc aca gaa cct cat att acc aac cct att 432
 Gln Leu Asn Cys Thr Leu Pro Thr Glu Pro His Ile Thr Asn Pro Ile
 130 135 140

gac ttc gag atc tgg ttt aaa cca cgc acc aga ttt ggg gat ttt ctt Asp Phe Glu Ile Trp Phe Lys Pro Arg Thr Arg Phe Gly Asp Phe Leu 145 150 155 160	480
ggg gat aaa gaa gac ttc gta ggg aat cat acc cgc acc agc ata tta Gly Asp Lys Glu Asp Phe Val Gly Asn His Thr Arg Thr Ser Ile Leu 165 170 175	528
cta ttt agc agc cgt aat ggg agt gtt aat tcc atg gat ctt ggg gac Leu Phe Ser Ser Arg Asn Gly Ser Val Asn Ser Met Asp Leu Gly Asp 180 185 190	576
gcg aca ctc ggg atc cta caa tct agg ata cca gat tac aca tta tat Ala Thr Leu Gly Ile Leu Gln Ser Arg Ile Pro Asp Tyr Thr Leu Tyr 195 200 205	624
aat att ccc ata caa cat acc gaa gcg atg tca ttg gga atc aaa tct Asn Ile Pro Ile Gln His Thr Glu Ala Met Ser Leu Gly Ile Lys Ser 210 215 220	672
gtg gaa tct gcc act tct ggt gtt tat aca tgg cgt gtc tat ggt gga Val Glu Ser Ala Thr Ser Gly Val Tyr Thr Trp Arg Val Tyr Gly Gly 225 230 235 240	720
gat ggt ctg aac aaa aca gtg ctg ggt cag gta aat gta tct gta gtg Asp Gly Leu Asn Lys Thr Val Leu Gly Gln Val Asn Val Ser Val Val 245 250 255	768
gca tat cac ccc ccg agc gta aat ctt aca cca cgc gcc agt cta ttt Ala Tyr His Pro Pro Ser Val Asn Leu Thr Pro Arg Ala Ser Leu Phe 260 265 270	816
aat aag acc ttt gag gcg gta tgt gca gtg gcg aat tac ttc ccc ccg Asn Lys Thr Phe Glu Ala Val Cys Ala Val Ala Asn Tyr Phe Pro Pro 275 280 285	864
cga tcc acg aaa cta aca tgg tat ctt gac ggg aag cca ata gaa agg Arg Ser Thr Lys Leu Thr Trp Tyr Leu Asp Gly Lys Pro Ile Glu Arg 290 295 300	912
caa tac att tca gat acg gca agt gta tgg ata gat gga ctc atc acc Gln Tyr Ile Ser Asp Thr Ala Ser Val Trp Ile Asp Gly Leu Ile Thr 305 310 315 320	960
aga agt tct gtg ttg gct att ccg aca act gaa aca gat tcc gag aaa Arg Ser Ser Val Leu Ala Ile Pro Thr Thr Glu Thr Asp Ser Glu Lys 325 330 335	1008
cca gat ata cga tgt gat ttg gaa tgg cat gaa agt cct gtg tcc tat Pro Asp Ile Arg Cys Asp Leu Glu Trp His Glu Ser Pro Val Ser Tyr 340 345 350	1056
aag aga ttc acg aaa agt gta gcc ccg gac gtc tat tac cca cct act Lys Arg Phe Thr Lys Ser Val Ala Pro Asp Val Tyr Tyr Pro Pro Thr 355 360 365	1104

gtg tct gtt acc ttc gct gat aca cgg gct ata tgt gat gtt aaa tgt 1152
 Val Ser Val Thr Phe Ala Asp Thr Arg Ala Ile Cys Asp Val Lys Cys
 370 375 380

gta cca cgg gac ggg ata tcc ttg atg tgg aaa att ggt aac tac cat 1200
 Val Pro Arg Asp Gly Ile Ser Leu Met Trp Lys Ile Gly Asn Tyr His
 385 390 395 400

cta cca aaa gca atg agt gct gat ata ctg atc aca ggt ccg tgt ata 1248
 Leu Pro Lys Ala Met Ser Ala Asp Ile Leu Ile Thr Gly Pro Cys Ile
 405 410 415

gaa cgt cca ggt ttg gtc aac att cag agt atg tgt gat ata tca gaa 1296
 Glu Arg Pro Gly Leu Val Asn Ile Gln Ser Met Cys Asp Ile Ser Glu
 420 425 430

acg gat gga ccc gtg agt tat acc tgt cag acc atc gga tac cca cca 1344
 Thr Asp Gly Pro Val Ser Tyr Thr Cys Gln Thr Ile Gly Tyr Pro Pro
 435 440 445

att cta ccg gga ttt tac gac aca caa gtc tac gac gcg tcc cct gaa 1392
 Ile Leu Pro Gly Phe Tyr Asp Thr Gln Val Tyr Asp Ala Ser Pro Glu
 450 455 460

atc gtc tcc
 Ile Val Ser 1401
 465

<210> 22
 <211> 467
 <212> PRT
 <213> Feline herpesvirus 1

<400> 22
 Met Ser Ile Glu Asn Ser Asp Asn Ser Thr Ala Glu Met Leu Ser Ser
 1 5 10 15
 Thr Ser Met Ser Ala Thr Thr Pro Ile Ser Gln Pro Thr Ser Pro Phe
 20 25 30
 Thr Thr Pro Thr Arg Arg Ser Thr Asn Ile Ala Thr Ser Ser Ser Thr
 35 40 45
 Thr Gln Ala Ser Gln Pro Thr Ser Thr Leu Thr Thr Leu Thr Arg Ser
 50 55 60
 Ser Thr Thr Ile Ala Thr Ser Pro Ser Thr Thr Gln Ala Ala Thr Phe
 65 70 75 80
 Ile Gly Ser Ser Thr Asp Ser Asn Thr Thr Leu Leu Lys Thr Thr Lys
 85 90 95
 Lys Pro Lys Arg Lys Lys Asn Lys Asn Asn Gly Ala Arg Phe Lys Leu
 100 105 110
 Asp Cys Gly Tyr Lys Gly Val Ile Tyr Arg Pro Tyr Phe Ser Pro Leu

115	120	125
Gln Leu Asn Cys Thr Leu Pro Thr Glu Pro His Ile Thr Asn Pro Ile		
130	135	140
Asp Phe Glu Ile Trp Phe Lys Pro Arg Thr Arg Phe Gly Asp Phe Leu		
145	150	155
Gly Asp Lys Glu Asp Phe Val Gly Asn His Thr Arg Thr Ser Ile Leu		
	165	170
Leu Phe Ser Ser Arg Asn Gly Ser Val Asn Ser Met Asp Leu Gly Asp		
	180	185
Ala Thr Leu Gly Ile Leu Gln Ser Arg Ile Pro Asp Tyr Thr Leu Tyr		
195	200	205
Asn Ile Pro Ile Gln His Thr Glu Ala Met Ser Leu Gly Ile Lys Ser		
210	215	220
Val Glu Ser Ala Thr Ser Gly Val Tyr Thr Trp Arg Val Tyr Gly Gly		
225	230	235
Asp Gly Leu Asn Lys Thr Val Leu Gly Gln Val Asn Val Ser Val Val		
	245	250
Ala Tyr His Pro Pro Ser Val Asn Leu Thr Pro Arg Ala Ser Leu Phe		
	260	265
Asn Lys Thr Phe Glu Ala Val Cys Ala Val Ala Asn Tyr Phe Pro Pro		
275	280	285
Arg Ser Thr Lys Leu Thr Trp Tyr Leu Asp Gly Lys Pro Ile Glu Arg		
290	295	300
Gln Tyr Ile Ser Asp Thr Ala Ser Val Trp Ile Asp Gly Leu Ile Thr		
305	310	315
Arg Ser Ser Val Leu Ala Ile Pro Thr Thr Glu Thr Asp Ser Glu Lys		
	325	330
Pro Asp Ile Arg Cys Asp Leu Glu Trp His Glu Ser Pro Val Ser Tyr		
	340	345
Lys Arg Phe Thr Lys Ser Val Ala Pro Asp Val Tyr Tyr Pro Pro Thr		
355	360	365
Val Ser Val Thr Phe Ala Asp Thr Arg Ala Ile Cys Asp Val Lys Cys		
370	375	380
Val Pro Arg Asp Gly Ile Ser Leu Met Trp Lys Ile Gly Asn Tyr His		
385	390	395
Leu Pro Lys Ala Met Ser Ala Asp Ile Leu Ile Thr Gly Pro Cys Ile		
	405	410
		415
Glu Arg Pro Gly Leu Val Asn Ile Gln Ser Met Cys Asp Ile Ser Glu		

130	135	140	
tat tgg ttg gaa cct tta aca aag tat atg ttc cta aca gac gat gaa Tyr Trp Leu Glu Pro Leu Thr Lys Tyr Met Phe Leu Thr Asp Asp Glu 145 150 155 160			480
ctg ggt ttg att atg atg gcc ccg gcc caa ttt aat caa gga caa tat Leu Gly Leu Ile Met Met Ala Pro Ala Gln Phe Asn Gln Gly Gln Tyr 165 170 175			528
cga aga gtt ata acc atc gat ggt tcc atg ttt tat aca gat ttt atg Arg Arg Val Ile Thr Ile Asp Gly Ser Met Phe Tyr Thr Asp Phe Met 180 185 190			576
gta caa cta tct cca acg cca tgt tgg ttc gca aaa ccc gat aga tac Val Gln Leu Ser Pro Thr Pro Cys Trp Phe Ala Lys Pro Asp Arg Tyr 195 200 205			624
gaa gag att cta cat gaa tgg tgt cga aat gtt aaa act att ggc ctt Glu Glu Ile Leu His Glu Trp Cys Arg Asn Val Lys Thr Ile Gly Leu 210 215 220			672
gat gga gct cgt gat tac cac tat tat tgg gta ccc tat aac cca caa Asp Gly Ala Arg Asp Tyr His Tyr Tyr Trp Val Pro Tyr Asn Pro Gln 225 230 235 240			720
cct cac cat aaa gcc gta ctc tta tat tgg tat cgg act cat ggc cga Pro His His Lys Ala Val Leu Leu Tyr Trp Tyr Arg Thr His Gly Arg 245 250 255			768
gaa ccc cca gta aga ttc caa gag gcc att cga tat gat cgt ccc gcc Glu Pro Pro Val Arg Phe Gln Glu Ala Ile Arg Tyr Asp Arg Pro Ala 260 265 270			816
ata ccg tct ggg agt gag gat tcg aaa cgg tcc aac gac tct aga gga Ile Pro Ser Gly Ser Glu Asp Ser Lys Arg Ser Asn Asp Ser Arg Gly 275 280 285			864
gaa tcg agt gga ccc aat tgg ata gac att gaa aat tac act cct aaa Glu Ser Ser Gly Pro Asn Trp Ile Asp Ile Glu Asn Tyr Thr Pro Lys 290 295 300			912
aat aat gtg cct att ata ata tct gac gat gac gtt cct aca gcc cct Asn Asn Val Pro Ile Ile Ile Ser Asp Asp Asp Val Pro Thr Ala Pro 305 310 315 320			960
ccc aag ggc atg aat aat cag tca gta gtg ata ccc gca atc gta cta Pro Lys Gly Met Asn Asn Gln Ser Val Val Ile Pro Ala Ile Val Leu 325 330 335			1008
agt tgt ctt ata ata gca ctg att cta gga gtg ata tat tat att ttg Ser Cys Leu Ile Ile Ala Leu Ile Leu Gly Val Ile Tyr Tyr Ile Leu 340 345 350			1056
agg gta aag agg tct cga tca act gca tat caa caa ctt cct ata ata Arg Val Lys Arg Ser Arg Ser Thr Ala Tyr Gln Gln Leu Pro Ile Ile 355 360 365			1104

cat aca act cac cat cct
His Thr Thr His His Pro
370

1122

<210> 24
<211> 374
<212> PRT
<213> Feline herpesvirus 1

<400> 24
Met Met Thr Arg Leu His Phe Trp Trp Cys Gly Ile Phe Ala Val Leu
1 5 10 15
Lys Tyr Leu Val Cys Thr Ser Ser Leu Thr Thr Thr Pro Lys Thr Thr
20 25 30
Thr Val Tyr Val Lys Gly Phe Asn Ile Pro Pro Leu Arg Tyr Asn Tyr
35 40 45
Thr Gln Ala Arg Ile Val Pro Lys Ile Pro Gln Ala Met Asp Pro Lys
50 55 60
Ile Thr Ala Glu Val Arg Tyr Val Thr Ser Met Asp Ser Cys Gly Met
65 70 75 80
Val Ala Leu Ile Ser Glu Pro Asp Ile Asp Ala Thr Ile Arg Thr Ile
85 90 95
Gln Leu Ser Gln Lys Lys Thr Tyr Asn Ala Thr Ile Ser Trp Phe Lys
100 105 110
Val Thr Gln Gly Cys Glu Tyr Pro Met Phe Leu Met Asp Met Arg Leu
115 120 125
Cys Asp Pro Lys Arg Glu Phe Gly Ile Cys Ala Leu Arg Ser Pro Ser
130 135 140
Tyr Trp Leu Glu Pro Leu Thr Lys Tyr Met Phe Leu Thr Asp Asp Glu
145 150 155 160
Leu Gly Leu Ile Met Met Ala Pro Ala Gln Phe Asn Gln Gly Gln Tyr
165 170 175
Arg Arg Val Ile Thr Ile Asp Gly Ser Met Phe Tyr Thr Asp Phe Met
180 185 190
Val Gln Leu Ser Pro Thr Pro Cys Trp Phe Ala Lys Pro Asp Arg Tyr
195 200 205
Glu Glu Ile Leu His Glu Trp Cys Arg Asn Val Lys Thr Ile Gly Leu
210 215 220
Asp Gly Ala Arg Asp Tyr His Tyr Tyr Trp Val Pro Tyr Asn Pro Gln
225 230 235 240

65	70	75	80	
agt tgg ttt aag gta acc cag ggt tgt gaa tac cct atg ttt ctt atg				288
Ser Trp Phe Lys Val Thr Gln Gly Cys Glu Tyr Pro Met Phe Leu Met	85	90	95	
gat atg aga ctt tgt gat cct aaa cgg gaa ttt gga ata tgt gct tta				336
Asp Met Arg Leu Cys Asp Pro Lys Arg Glu Phe Gly Ile Cys Ala Leu	100	105	110	
cgg tcg cct tca tat tgg ttg gaa cct tta aca aag tat atg ttc cta				384
Arg Ser Pro Ser Tyr Trp Leu Glu Pro Leu Thr Lys Tyr Met Phe Leu	115	120	125	
aca gac gat gaa ctg ggt ttg att atg atg gcc ccg gcc caa ttt aat				432
Thr Asp Asp Glu Leu Gly Leu Ile Met Met Ala Pro Ala Gln Phe Asn	130	135	140	
caa gga caa tat cga aga gtt ata acc atc gat ggt tcc atg ttt tat				480
Gln Gly Gln Tyr Arg Arg Val Ile Thr Ile Asp Gly Ser Met Phe Tyr	145	150	155	160
aca gat ttt atg gta caa cta tct cca acg cca tgt tgg ttc gca aaa				528
Thr Asp Phe Met Val Gln Leu Ser Pro Thr Pro Cys Trp Phe Ala Lys	165	170	175	
ccc gat aga tac gaa gag att cta cat gaa tgg tgt cga aat gtt aaa				576
Pro Asp Arg Tyr Glu Glu Ile Leu His Glu Trp Cys Arg Asn Val Lys	180	185	190	
act att ggc ctt gat gga gct cgt gat tac cac tat tat tgg gta ccc				624
Thr Ile Gly Leu Asp Gly Ala Arg Asp Tyr His Tyr Tyr Trp Val Pro	195	200	205	
tat aac cca caa cct cac cat aaa gcc gta ctc tta tat tgg tat cgg				672
Tyr Asn Pro Gln Pro His His Lys Ala Val Leu Leu Tyr Trp Tyr Arg	210	215	220	
act cat ggc cga gaa ccc cca gta aga ttc caa gag gcc att cga tat				720
Thr His Gly Arg Glu Pro Pro Val Arg Phe Gln Glu Ala Ile Arg Tyr	225	230	235	240
gat cgt ccc gcc ata ccg tct ggg agt gag gat tcg aaa cgg tcc aac				768
Asp Arg Pro Ala Ile Pro Ser Gly Ser Glu Asp Ser Lys Arg Ser Asn	245	250	255	
gac tct aga gga gaa tcg agt gga ccc aat tgg ata gac att gaa aat				816
Asp Ser Arg Gly Glu Ser Ser Gly Pro Asn Trp Ile Asp Ile Glu Asn	260	265	270	
tac act cct aaa aat aat gtg cct att ata ata tct gac gat gac gtt				864
Tyr Thr Pro Lys Asn Asn Val Pro Ile Ile Ile Ser Asp Asp Asp Val	275	280	285	
cct aca gcc cct ccc aag ggc atg aat aat cag tca				900
Pro Thr Ala Pro Pro Lys Gly Met Asn Asn Gln Ser	290	295	300	

<210> 26
 <211> 300
 <212> PRT
 <213> Feline herpesvirus 1

 <400> 26
 Pro Lys Thr Thr Thr Val Tyr Val Lys Gly Phe Asn Ile Pro Pro Leu
 1 5 10 15
 Arg Tyr Asn Tyr Thr Gln Ala Arg Ile Val Pro Lys Ile Pro Gln Ala
 20 25 30
 Met Asp Pro Lys Ile Thr Ala Glu Val Arg Tyr Val Thr Ser Met Asp
 35 40 45
 Ser Cys Gly Met Val Ala Leu Ile Ser Glu Pro Asp Ile Asp Ala Thr
 50 55 60
 Ile Arg Thr Ile Gln Leu Ser Gln Lys Lys Thr Tyr Asn Ala Thr Ile
 65 70 75 80
 Ser Trp Phe Lys Val Thr Gln Gly Cys Glu Tyr Pro Met Phe Leu Met
 85 90 95
 Asp Met Arg Leu Cys Asp Pro Lys Arg Glu Phe Gly Ile Cys Ala Leu
 100 105 110
 Arg Ser Pro Ser Tyr Trp Leu Glu Pro Leu Thr Lys Tyr Met Phe Leu
 115 120 125
 Thr Asp Asp Glu Leu Gly Leu Ile Met Met Ala Pro Ala Gln Phe Asn
 130 135 140
 Gln Gly Gln Tyr Arg Arg Val Ile Thr Ile Asp Gly Ser Met Phe Tyr
 145 150 155 160
 Thr Asp Phe Met Val Gln Leu Ser Pro Thr Pro Cys Trp Phe Ala Lys
 165 170 175
 Pro Asp Arg Tyr Glu Glu Ile Leu His Glu Trp Cys Arg Asn Val Lys
 180 185 190
 Thr Ile Gly Leu Asp Gly Ala Arg Asp Tyr His Tyr Tyr Trp Val Pro
 195 200 205
 Tyr Asn Pro Gln Pro His His Lys Ala Val Leu Leu Tyr Trp Tyr Arg
 210 215 220
 Thr His Gly Arg Glu Pro Pro Val Arg Phe Gln Glu Ala Ile Arg Tyr
 225 230 235 240
 Asp Arg Pro Ala Ile Pro Ser Gly Ser Glu Asp Ser Lys Arg Ser Asn
 245 250 255
 Asp Ser Arg Gly Glu Ser Ser Gly Pro Asn Trp Ile Asp Ile Glu Asn

260 265 270
 Tyr Thr Pro Lys Asn Asn Val Pro Ile Ile Ile Ser Asp Asp Asp Val
 275 280 285
 Pro Thr Ala Pro Pro Lys Gly Met Asn Asn Gln Ser
 290 295 300

 <210> 27
 <211> 759
 <212> DNA
 <213> Feline leukemia virus

 <220>
 <221> CDS
 <222> (1)..(759)

 <400> 27
 atg ccg ctg cgt gaa ggt ccg aac aac cgt ccc cag tat tgg cca ttc 48
 Met Pro Leu Arg Glu Gly Pro Asn Asn Arg Pro Gln Tyr Trp Pro Phe
 1 5 10 15
 tca gct tca gac ctg tat aac tgg aag tcg cat aac ccc cct ttc tcc 96
 Ser Ala Ser Asp Leu Tyr Asn Trp Lys Ser His Asn Pro Pro Phe Ser
 20 25 30
 caa gac ccc gtg gcc cta act aac cta att gag tcc att tta gtg acg 144
 Gln Asp Pro Val Ala Leu Thr Asn Leu Ile Glu Ser Ile Leu Val Thr
 35 40 45
 cat caa cca acc tgg gac gac tgc cag caa ctc ttg cag gca ctc ctg 192
 His Gln Pro Thr Trp Asp Asp Cys Gln Gln Leu Leu Gln Ala Leu Leu
 50 55 60
 aca ggc gaa gaa agg caa agg gtc ctt ctt gag gcc cga aag cag gtt 240
 Thr Gly Glu Glu Arg Gln Arg Val Leu Leu Glu Ala Arg Lys Gln Val
 65 70 75 80
 cca ggc gag gac gga cgg cca acc cag ctg ccc aat gtc att gac gaa 288
 Pro Gly Glu Asp Gly Arg Pro Thr Gln Leu Pro Asn Val Ile Asp Glu
 85 90 95
 gct ttc ccc ttg acc cgt ccc aac tgg gat ttt gct acg ccg gca ggt 336
 Ala Phe Pro Leu Thr Arg Pro Asn Trp Asp Phe Ala Thr Pro Ala Gly
 100 105 110
 agg gag cac cta cgc ctt tat cgc cag ttg ctg tta gcg ggt ctc cgc 384
 Arg Glu His Leu Arg Leu Tyr Arg Gln Leu Leu Leu Ala Gly Leu Arg
 115 120 125
 ggg gct gca aga cgc ccc act aat ttg gca cag gta aag caa gtt gta 432
 Gly Ala Ala Arg Arg Pro Thr Asn Leu Ala Gln Val Lys Gln Val Val
 130 135 140
 caa ggg aaa gag gaa acg cca gcc tca ttc tta gaa aga tta aaa gag 480

Gln Gly Lys Glu Glu Thr Pro Ala Ser Phe Leu Glu Arg Leu Lys Glu
 145 150 155 160
 gct tac aga atg tat act ccc tat gac cct gag gac cca ggg cag gct 528
 Ala Tyr Arg Met Tyr Thr Pro Tyr Asp Pro Glu Asp Pro Gly Gln Ala
 165 170 175
 gct agt gtt atc ctg tcc ttt atc tac cag tct agc ccg gac ata aga 576
 Ala Ser Val Ile Leu Ser Phe Ile Tyr Gln Ser Ser Pro Asp Ile Arg
 180 185 190
 aat aag tta caa agg cta gaa ggc cta cag ggg ttc aca ctg tct gat 624
 Asn Lys Leu Gln Arg Leu Glu Gly Leu Gln Gly Phe Thr Leu Ser Asp
 195 200 205
 ttg cta aaa gag gca gaa aag ata tac aac aaa agg gag acc cca gag 672
 Leu Leu Lys Glu Ala Glu Lys Ile Tyr Asn Lys Arg Glu Thr Pro Glu
 210 215 220
 gaa agg gaa gaa aga tta tgg cag cgg cag gaa gaa aga gat aaa aag 720
 Glu Arg Glu Glu Arg Leu Trp Gln Arg Gln Glu Glu Arg Asp Lys Lys
 225 230 235 240
 cgc cat aag gag atg act aag gtc tgt gag aat tct agc 759
 Arg His Lys Glu Met Thr Lys Val Cys Glu Asn Ser Ser
 245 250

 <210> 28
 <211> 253
 <212> PRT
 <213> Feline leukemia virus

 <400> 28
 Met Pro Leu Arg Glu Gly Pro Asn Asn Arg Pro Gln Tyr Trp Pro Phe
 1 5 10 15
 Ser Ala Ser Asp Leu Tyr Asn Trp Lys Ser His Asn Pro Pro Phe Ser
 20 25 30
 Gln Asp Pro Val Ala Leu Thr Asn Leu Ile Glu Ser Ile Leu Val Thr
 35 40 45
 His Gln Pro Thr Trp Asp Asp Cys Gln Gln Leu Leu Gln Ala Leu Leu
 50 55 60
 Thr Gly Glu Glu Arg Gln Arg Val Leu Leu Glu Ala Arg Lys Gln Val
 65 70 75 80
 Pro Gly Glu Asp Gly Arg Pro Thr Gln Leu Pro Asn Val Ile Asp Glu
 85 90 95
 Ala Phe Pro Leu Thr Arg Pro Asn Trp Asp Phe Ala Thr Pro Ala Gly
 100 105 110
 Arg Glu His Leu Arg Leu Tyr Arg Gln Leu Leu Leu Ala Gly Leu Arg
 115 120 125

Gly Ala Ala Arg Arg Pro Thr Asn Leu Ala Gln Val Lys Gln Val Val
 130 135 140
 Gln Gly Lys Glu Glu Thr Pro Ala Ser Phe Leu Glu Arg Leu Lys Glu
 145 150 155 160
 Ala Tyr Arg Met Tyr Thr Pro Tyr Asp Pro Glu Asp Pro Gly Gln Ala
 165 170 175
 Ala Ser Val Ile Leu Ser Phe Ile Tyr Gln Ser Ser Pro Asp Ile Arg
 180 185 190
 Asn Lys Leu Gln Arg Leu Glu Gly Leu Gln Gly Phe Thr Leu Ser Asp
 195 200 205
 Leu Leu Lys Glu Ala Glu Lys Ile Tyr Asn Lys Arg Glu Thr Pro Glu
 210 215 220
 Glu Arg Glu Glu Arg Leu Trp Gln Arg Gln Glu Glu Arg Asp Lys Lys
 225 230 235 240
 Arg His Lys Glu Met Thr Lys Val Cys Glu Asn Ser Ser
 245 250

<210> 29
 <211> 1830
 <212> DNA
 <213> Feline leukemia virus

<220>
 <221> CDS
 <222> (1)..(1830)

<400> 29
 atg gcc aat cct agt cca ccc caa atg tat aat gta act tgg gta ata 48
 Met Ala Asn Pro Ser Pro Pro Gln Met Tyr Asn Val Thr Trp Val Ile
 1 5 10 15
 acc aat gta caa acc aac acc caa gct aat gcc acc tct atg tta gga 96
 Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr Ser Met Leu Gly
 20 25 30
 acc tta acc gat gtc tac cct acc cta cat gtt gac tta tgt gac cta 144
 Thr Leu Thr Asp Val Tyr Pro Thr Leu His Val Asp Leu Cys Asp Leu
 35 40 45
 gtg gga gac acc tgg gaa cct atg gtc cta agc cca acc ggg tac cct 192
 Val Gly Asp Thr Trp Glu Pro Met Val Leu Ser Pro Thr Gly Tyr Pro
 50 55 60
 ccc tca aaa tat gga tgt aaa act aca gat aga aaa aaa cag caa cag 240
 Pro Ser Lys Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln
 65 70 75 80

aca tac ccc ttt tac gtc tgc ccc ggg cat cgc ccc tcg ctg ggg cca	288
Thr Tyr Pro Phe Val Cys Pro Gly His Arg Pro Ser Leu Gly Pro	
85 90 95	
aag gga aca cat tgt gga ggg gca caa gat ggg ttt tgt gcc gca tgg	336
Lys Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp	
100 105 110	
gga tgt gaa acc acc gga gaa gct tgg tgg aag ccc tcc tcc tca tgg	384
Gly Cys Glu Thr Thr Gly Glu Ala Trp Trp Lys Pro Ser Ser Ser Trp	
115 120 125	
gac tat atc aca gta aaa aga ggg agt agt cag aac aat aac tgt gag	432
Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asn Asn Asn Cys Glu	
130 135 140	
gga aaa tgc aac ccc ctg att ttg cag ttc acc cag aag ggg aaa caa	480
Gly Lys Cys Asn Pro Leu Ile Leu Gln Phe Thr Gln Lys Gly Lys Gln	
145 150 155 160	
gcc tct tgg gac gga cct aag atg tgg gga ttg cgg cta tac cgt aca	528
Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg Leu Tyr Arg Thr	
165 170 175	
gga tat gac cct atc gcc tta ttc acg gta tcc cgg cgg gtg tca acc	576
Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser Arg Arg Val Ser Thr	
180 185 190	
att acg ccg cct cag gca atg gga cca gac cta gtc tta cct gat caa	624
Ile Thr Pro Pro Gln Ala Met Gly Pro Asp Leu Val Leu Pro Asp Gln	
195 200 205	
aaa ccc cca tcc cga caa tct caa aca ggg tcc aaa gtg gcg acc cag	672
Lys Pro Pro Ser Arg Gln Ser Gln Thr Gly Ser Lys Val Ala Thr Gln	
210 215 220	
agg ccc caa acg aat gaa agc gcc cca agg tct gtt gcc ccc acc acc	720
Arg Pro Gln Thr Asn Glu Ser Ala Pro Arg Ser Val Ala Pro Thr Thr	
225 230 235 240	
gtg ggt ccc aaa cgg att ggg acc gga gat agg tta ata aat tta gta	768
Val Gly Pro Lys Arg Ile Gly Thr Gly Asp Arg Leu Ile Asn Leu Val	
245 250 255	
caa ggg gca tac cta gcc tta aat gcc acc gac ccc aac aaa act aaa	816
Gln Gly Ala Tyr Leu Ala Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys	
260 265 270	
gac tgt tgg ctc tgc ctg gtt tct cga cca ccc tat tac gaa ggg att	864
Asp Cys Trp Leu Cys Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile	
275 280 285	
gca atc tta ggt aac tac agc aac caa aca aac cct ccc cca tcc tgc	912
Ala Ile Leu Gly Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys	
290 295 300	
cta tct att ccg cca cac aag ctg acc ata tct aaa gta tca ggg caa	960

Leu Ser Ile Pro Pro His Lys Leu Thr Ile Ser Lys Val Ser Gly Gln	
305 310 315 320	
gga ctg tgc ata ggg act gtt cct aag acc cac cag gct ttg tgc aat	1008
Gly Leu Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn	
325 330 335	
aag acg cac cag gga cat aca ggg gcg gac tat cga gcc gcc ccg cgg	1056
Lys Thr His Gln Gly His Thr Gly Ala Asp Tyr Arg Ala Ala Pro Arg	
340 345 350	
tat cta gcc gcc ccc aat ggc acc tat tgg gcc tgt aac act gga ctc	1104
Tyr Leu Ala Ala Pro Asn Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu	
355 360 365	
acc cca tgc att tcc atg gcg gtg ctc aat ttg acc tct gat ttt tgt	1152
Thr Pro Cys Ile Ser Met Ala Val Leu Asn Leu Thr Ser Asp Phe Cys	
370 375 380	
gtc tta atc gaa tta tgg ccc aga gtg act tac cat caa ccc gaa tat	1200
Val Leu Ile Glu Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr	
385 390 395 400	
gtg tac aca cat ttt gcc aaa gct ggc agg ttc cga aga gaa cca ata	1248
Val Tyr Thr His Phe Ala Lys Ala Gly Arg Phe Arg Arg Glu Pro Ile	
405 410 415	
tca cta act gtt gcc ctc atg ttg gga gga ctc act gta ggg ggc ata	1296
Ser Leu Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile	
420 425 430	
gcc gcg ggg gtc gga aca ggg act aaa gcc ctc ctt gaa aca gcc cag	1344
Ala Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln	
435 440 445	
ttc aga caa cta caa atg gcc atg cac aca gac atc cag gcc cta gaa	1392
Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu Glu	
450 455 460	
gag tca att agt gcc tta gaa aag tcc ctg acc tcc ctt tct gaa gta	1440
Glu Ser Ile Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser Glu Val	
465 470 475 480	
gtc tta caa aac aga cgg ggc cta gat att cta ttc cta caa gag gga	1488
Val Leu Gln Asn Arg Arg Gly Leu Asp Ile Leu Phe Leu Gln Glu Gly	
485 490 495	
ggg ctc tgt gcc gca tta aaa gaa gaa tgt tgc ttc tat gcg gat cac	1536
Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ala Asp His	
500 505 510	
acc gga ctc gtc cga gac aat atg gct aaa tta aga gaa aga cta aaa	1584
Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu Arg Glu Arg Leu Lys	
515 520 525	
cag cgg caa caa ctg ttt gac tcc caa cag gga tgg ttt gaa gga tgg	1632
Gln Arg Gln Gln Leu Phe Asp Ser Gln Gln Gly Trp Phe Glu Gly Trp	

530	535	540	
ttc aac agg tcc ccc tgg ttt aca acc cta att tcc tcc att atg ggc			1680
Phe Asn Arg Ser Pro Trp Phe Thr Thr Leu Ile Ser Ser Ile Met Gly			
545	550	555	560
ccc tta cta atc cta ctc cta att ctc ctc ttc ggc cca tac atc ctt			1728
Pro Leu Leu Ile Leu Leu Leu Ile Leu Leu Phe Gly Pro Tyr Ile Leu			
	565	570	575
aac aga tta gta caa ttc gta aaa gac aga ata tct gtg gta caa gcc			1776
Asn Arg Leu Val Gln Phe Val Lys Asp Arg Ile Ser Val Val Gln Ala			
	580	585	590
tta att tta acc caa cag tac caa cag ata aag caa tac gat ccg gac			1824
Leu Ile Leu Thr Gln Gln Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp			
	595	600	605
cga cca			
Arg Pro			1830
610			
<210> 30			
<211> 610			
<212> PRT			
<213> Feline leukemia virus			
<400> 30			
Met Ala Asn Pro Ser Pro Pro Gln Met Tyr Asn Val Thr Trp Val Ile			
1	5	10	15
Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr Ser Met Leu Gly			
	20	25	30
Thr Leu Thr Asp Val Tyr Pro Thr Leu His Val Asp Leu Cys Asp Leu			
	35	40	45
Val Gly Asp Thr Trp Glu Pro Met Val Leu Ser Pro Thr Gly Tyr Pro			
	50	55	60
Pro Ser Lys Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln			
	65	70	75
Thr Tyr Pro Phe Tyr Val Cys Pro Gly His Arg Pro Ser Leu Gly Pro			
	85	90	95
Lys Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp			
	100	105	110
Gly Cys Glu Thr Thr Gly Glu Ala Trp Trp Lys Pro Ser Ser Ser Trp			
	115	120	125
Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asn Asn Asn Cys Glu			
	130	135	140
Gly Lys Cys Asn Pro Leu Ile Leu Gln Phe Thr Gln Lys Gly Lys Gln			

145	150	155	160
Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg Leu Tyr Arg Thr			
	165	170	175
Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser Arg Arg Val Ser Thr			
	180	185	190
Ile Thr Pro Pro Gln Ala Met Gly Pro Asp Leu Val Leu Pro Asp Gln			
	195	200	205
Lys Pro Pro Ser Arg Gln Ser Gln Thr Gly Ser Lys Val Ala Thr Gln			
	210	215	220
Arg Pro Gln Thr Asn Glu Ser Ala Pro Arg Ser Val Ala Pro Thr Thr			
	225	230	235
Val Gly Pro Lys Arg Ile Gly Thr Gly Asp Arg Leu Ile Asn Leu Val			
	245	250	255
Gln Gly Ala Tyr Leu Ala Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys			
	260	265	270
Asp Cys Trp Leu Cys Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile			
	275	280	285
Ala Ile Leu Gly Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys			
	290	295	300
Leu Ser Ile Pro Pro His Lys Leu Thr Ile Ser Lys Val Ser Gly Gln			
	305	310	315
Gly Leu Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn			
	325	330	335
Lys Thr His Gln Gly His Thr Gly Ala Asp Tyr Arg Ala Ala Pro Arg			
	340	345	350
Tyr Leu Ala Ala Pro Asn Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu			
	355	360	365
Thr Pro Cys Ile Ser Met Ala Val Leu Asn Leu Thr Ser Asp Phe Cys			
	370	375	380
Val Leu Ile Glu Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr			
	385	390	395
Val Tyr Thr His Phe Ala Lys Ala Gly Arg Phe Arg Arg Glu Pro Ile			
	405	410	415
Ser Leu Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile			
	420	425	430
Ala Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln			
	435	440	445
Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu Glu			

450 455 460
 Glu Ser Ile Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser Glu Val
 465 470 475 480
 Val Leu Gln Asn Arg Arg Gly Leu Asp Ile Leu Phe Leu Gln Glu Gly
 485 490 495
 Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ala Asp His
 500 505 510
 Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu Arg Glu Arg Leu Lys
 515 520 525
 Gln Arg Gln Gln Leu Phe Asp Ser Gln Gln Gly Trp Phe Glu Gly Trp
 530 535 540
 Phe Asn Arg Ser Pro Trp Phe Thr Thr Leu Ile Ser Ser Ile Met Gly
 545 550 555 560
 Pro Leu Leu Ile Leu Leu Leu Ile Leu Leu Phe Gly Pro Tyr Ile Leu
 565 570 575
 Asn Arg Leu Val Gln Phe Val Lys Asp Arg Ile Ser Val Val Gln Ala
 580 585 590
 Leu Ile Leu Thr Gln Gln Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp
 595 600 605
 Arg Pro
 610

<210> 31
 <211> 1833
 <212> DNA
 <213> Feline leukemia virus

<220>
 <221> CDS
 <222> (1)..(1833)

<400> 31
 atg gag cac cta cgc ctt tat cgc cag ttg ctg tta gcg ggt ctc cgc 48
 Met Glu His Leu Arg Leu Tyr Arg Gln Leu Leu Leu Ala Gly Leu Arg
 1 5 10 15
 ggg gct gca aga cac ccc act aat ttg gca cag gtt aag caa ttt tta 96
 Gly Ala Ala Arg His Pro Thr Asn Leu Ala Gln Val Lys Gln Phe Leu
 20 25 30
 caa ggg aaa gaa gaa acg cca gcc tca ttc tta gaa aga tta aaa gag 144
 Gln Gly Lys Glu Glu Thr Pro Ala Ser Phe Leu Glu Arg Leu Lys Glu
 35 40 45
 gct tac cga atg tat act ccc tat gac cct gag gac cca ggg cag gct 192

Ala Tyr Arg Met Tyr Thr Pro Tyr Asp Pro Glu Asp Pro Gly Gln Ala	
50 55 60	
gct agt gtt atc ctg tcc ttt atc tac cag tct agc ccg gac ata aga	240
Ala Ser Val Ile Leu Ser Phe Ile Tyr Gln Ser Ser Pro Asp Ile Arg	
65 70 75 80	
aat aag tta caa agg cta gaa ggc cta cag ggg ttc aca ctg tct gat	288
Asn Lys Leu Gln Arg Leu Glu Gly Leu Gln Gly Phe Thr Leu Ser Asp	
85 90 95	
ttg cta aaa gag gca gaa aag ata tac aac aaa agg gag acc cca gag	336
Leu Leu Lys Glu Ala Glu Lys Ile Tyr Asn Lys Arg Glu Thr Pro Glu	
100 105 110	
gaa agg gaa gaa aga tta tgg cag cgg cag gaa gaa aga gat aaa aag	384
Glu Arg Glu Glu Arg Leu Trp Gln Arg Gln Glu Glu Arg Asp Lys Lys	
115 120 125	
cgc cat aag gag atg act aaa gtt ctg gcc aca gta gtt gct cag aat	432
Arg His Lys Glu Met Thr Lys Val Leu Ala Thr Val Val Ala Gln Asn	
130 135 140	
aga gat aag gat aga gag gaa agt aaa ctg gga gat caa aga aaa ata	480
Arg Asp Lys Asp Arg Glu Glu Ser Lys Leu Gly Asp Gln Arg Lys Ile	
145 150 155 160	
cct ctg ggg aaa gac cag tgt gcc tat tgc aag gaa aag gga cat tgg	528
Pro Leu Gly Lys Asp Gln Cys Ala Tyr Cys Lys Glu Lys Gly His Trp	
165 170 175	
gtt cgc gat tgc ccc aac cgg ccc cgg aag aaa ccc gcc aac tcc act	576
Val Arg Asp Cys Pro Asn Arg Pro Arg Lys Lys Pro Ala Asn Ser Thr	
180 185 190	
ctc ctc aac tta gaa gat atg gcc aat cct agt cca ccc caa atg tat	624
Leu Leu Asn Leu Glu Asp Met Ala Asn Pro Ser Pro Pro Gln Met Tyr	
195 200 205	
aat gta act tgg gta ata acc aat gta caa acc aac acc caa gct aat	672
Asn Val Thr Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn	
210 215 220	
gcc acc tct atg tta gga acc tta acc gat gtc tac cct acc cta cat	720
Ala Thr Ser Met Leu Gly Thr Leu Thr Asp Val Tyr Pro Thr Leu His	
225 230 235 240	
gtt gac tta tgt gac cta gtg gga gac acc tgg gaa cct atg gtc cta	768
Val Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Met Val Leu	
245 250 255	
agc cca acc ggg tac cct ccc tca aaa tat gga tgt aaa act aca gat	816
Ser Pro Thr Gly Tyr Pro Pro Ser Lys Tyr Gly Cys Lys Thr Thr Asp	
260 265 270	
aga aaa aaa cag caa cag aca tac ccc ttt tac gtc tgc ccc ggg cat	864
Arg Lys Lys Gln Gln Gln Thr Tyr Pro Phe Tyr Val Cys Pro Gly His	

275	280	285	
cgc ccc tcg ctg ggg cca aag gga aca cat tgt gga ggg gca caa gat Arg Pro Ser Leu Gly Pro Lys Gly Thr His Cys Gly Gly Ala Gln Asp 290 295 300			912
ggg ttt tgt gcc gca tgg gga tgt gaa acc acc gga gaa gct tgg tgg Gly Phe Cys Ala Ala Trp Gly Cys Glu Thr Thr Gly Glu Ala Trp Trp 305 310 315 320			960
aag ccc tcc tcc tca tgg gac tat atc aca gta aaa aga ggg agt agt Lys Pro Ser Ser Ser Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser 325 330 335			1008
cag aac aat aac tgt gag gga aaa tgc aac ccc ctg att ttg cag ttc Gln Asn Asn Asn Cys Glu Gly Lys Cys Asn Pro Leu Ile Leu Gln Phe 340 345 350			1056
acc cag aag ggg aaa caa gcc tct tgg gac gga cct aag atg tgg gga Thr Gln Lys Gly Lys Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly 355 360 365			1104
ttg cgg cta tac cgt aca gga tat gac cct atc gcc tta ttc acg gta Leu Arg Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val 370 375 380			1152
tcc cgg cgg gtg tca acc att acg ccg cct cag gca atg gga cca gac Ser Arg Arg Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asp 385 390 395 400			1200
cta gtc tta cct gat caa aaa ccc cca tcc cga caa tct caa aca ggg Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr Gly 405 410 415			1248
tcc aaa gtg gcg acc cag agg ccc caa acg aat gaa agc gcc cca agg Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala Pro Arg 420 425 430			1296
tct gtt gcc ccc acc acc gtg ggt ccc aaa cgg att ggg acc gga gat Ser Val Ala Pro Thr Thr Val Gly Pro Lys Arg Ile Gly Thr Gly Asp 435 440 445			1344
agg tta ata aat tta gta caa ggg gca tac cta gcc tta aat gcc acc Arg Leu Ile Asn Leu Val Gln Gly Ala Tyr Leu Ala Leu Asn Ala Thr 450 455 460			1392
gac ccc aac aaa act aaa gac tgt tgg ctc tgc ctg gtt tct cga cca Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys Leu Val Ser Arg Pro 465 470 475 480			1440
ccc tat tac gaa ggg att gca atc tta ggt aac tac agc aac caa aca Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly Asn Tyr Ser Asn Gln Thr 485 490 495			1488
aac cct ccc cca tcc tgc cta tct att ccg cca cac aag ctg acc ata Asn Pro Pro Pro Ser Cys Leu Ser Ile Pro Pro His Lys Leu Thr Ile 500 505 510			1536

tct aaa gta tca ggg caa gga ctg tgc ata ggg act gtt cct aag acc	1584
Ser Lys Val Ser Gly Gln Gly Leu Cys Ile Gly Thr Val Pro Lys Thr	
515 520 525	
cac cag gct ttg tgc aat aag acg cac cag gga cat aca ggg gcg gac	1632
His Gln Ala Leu Cys Asn Lys Thr His Gln Gly His Thr Gly Ala Asp	
530 535 540	
tat cga gcc gcc ccg cgg tat cta gcc gcc ccc aat ggc acc tat tgg	1680
Tyr Arg Ala Ala Pro Arg Tyr Leu Ala Ala Pro Asn Gly Thr Tyr Trp	
545 550 555 560	
gcc tgt aac act gga ctc acc cca tgc att tcc atg gcg gtg ctc aat	1728
Ala Cys Asn Thr Gly Leu Thr Pro Cys Ile Ser Met Ala Val Leu Asn	
565 570 575	
ttg acc tct gat ttt tgt gtc tta atc gaa tta tgg ccc aga gtg act	1776
Leu Thr Ser Asp Phe Cys Val Leu Ile Glu Leu Trp Pro Arg Val Thr	
580 585 590	
tac cat caa ccc gaa tat gtg tac aca cat ttt gcc aaa gct ggc agg	1824
Tyr His Gln Pro Glu Tyr Val Tyr Thr His Phe Ala Lys Ala Gly Arg	
595 600 605	
ttc cga aga	
Phe Arg Arg	1833
610	
<210> 32	
<211> 611	
<212> PRT	
<213> Feline leukemia virus	
<400> 32	
Met Glu His Leu Arg Leu Tyr Arg Gln Leu Leu Leu Ala Gly Leu Arg	
1 5 10 15	
Gly Ala Ala Arg His Pro Thr Asn Leu Ala Gln Val Lys Gln Phe Leu	
20 25 30	
Gln Gly Lys Glu Glu Thr Pro Ala Ser Phe Leu Glu Arg Leu Lys Glu	
35 40 45	
Ala Tyr Arg Met Tyr Thr Pro Tyr Asp Pro Glu Asp Pro Gly Gln Ala	
50 55 60	
Ala Ser Val Ile Leu Ser Phe Ile Tyr Gln Ser Ser Pro Asp Ile Arg	
65 70 75 80	
Asn Lys Leu Gln Arg Leu Glu Gly Leu Gln Gly Phe Thr Leu Ser Asp	
85 90 95	
Leu Leu Lys Glu Ala Glu Lys Ile Tyr Asn Lys Arg Glu Thr Pro Glu	
100 105 110	

Glu Arg Glu Glu Arg Leu Trp Gln Arg Gln Glu Glu Arg Asp Lys Lys
 115 120 125
 Arg His Lys Glu Met Thr Lys Val Leu Ala Thr Val Val Ala Gln Asn
 130 135 140
 Arg Asp Lys Asp Arg Glu Glu Ser Lys Leu Gly Asp Gln Arg Lys Ile
 145 150 155 160
 Pro Leu Gly Lys Asp Gln Cys Ala Tyr Cys Lys Glu Lys Gly His Trp
 165 170 175
 Val Arg Asp Cys Pro Asn Arg Pro Arg Lys Lys Pro Ala Asn Ser Thr
 180 185 190
 Leu Leu Asn Leu Glu Asp Met Ala Asn Pro Ser Pro Pro Gln Met Tyr
 195 200 205
 Asn Val Thr Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn
 210 215 220
 Ala Thr Ser Met Leu Gly Thr Leu Thr Asp Val Tyr Pro Thr Leu His
 225 230 235 240
 Val Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Met Val Leu
 245 250 255
 Ser Pro Thr Gly Tyr Pro Pro Ser Lys Tyr Gly Cys Lys Thr Thr Asp
 260 265 270
 Arg Lys Lys Gln Gln Gln Thr Tyr Pro Phe Tyr Val Cys Pro Gly His
 275 280 285
 Arg Pro Ser Leu Gly Pro Lys Gly Thr His Cys Gly Gly Ala Gln Asp
 290 295 300
 Gly Phe Cys Ala Ala Trp Gly Cys Glu Thr Thr Gly Glu Ala Trp Trp
 305 310 315 320
 Lys Pro Ser Ser Ser Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser
 325 330 335
 Gln Asn Asn Asn Cys Glu Gly Lys Cys Asn Pro Leu Ile Leu Gln Phe
 340 345 350
 Thr Gln Lys Gly Lys Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly
 355 360 365
 Leu Arg Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val
 370 375 380
 Ser Arg Arg Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asp
 385 390 395 400
 Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr Gly
 405 410 415

Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala Pro Arg
 420 425 430
 Ser Val Ala Pro Thr Thr Val Gly Pro Lys Arg Ile Gly Thr Gly Asp
 435 440 445
 Arg Leu Ile Asn Leu Val Gln Gly Ala Tyr Leu Ala Leu Asn Ala Thr
 450 455 460
 Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys Leu Val Ser Arg Pro
 465 470 475 480
 Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly Asn Tyr Ser Asn Gln Thr
 485 490 495
 Asn Pro Pro Pro Ser Cys Leu Ser Ile Pro Pro His Lys Leu Thr Ile
 500 505 510
 Ser Lys Val Ser Gly Gln Gly Leu Cys Ile Gly Thr Val Pro Lys Thr
 515 520 525
 His Gln Ala Leu Cys Asn Lys Thr His Gln Gly His Thr Gly Ala Asp
 530 535 540
 Tyr Arg Ala Ala Pro Arg Tyr Leu Ala Ala Pro Asn Gly Thr Tyr Trp
 545 550 555 560
 Ala Cys Asn Thr Gly Leu Thr Pro Cys Ile Ser Met Ala Val Leu Asn
 565 570 575
 Leu Thr Ser Asp Phe Cys Val Leu Ile Glu Leu Trp Pro Arg Val Thr
 580 585 590
 Tyr His Gln Pro Glu Tyr Val Tyr Thr His Phe Ala Lys Ala Gly Arg
 595 600 605
 Phe Arg Arg
 610

<210> 33
 <211> 1812
 <212> DNA
 <213> canine distemper virus

<220>
 <221> CDS
 <222> (1)..(1812)

<400> 33
 atg ctc ccc tac caa gac aag gtg ggt gcc ttc tac aag gat aat gca 48
 Met Leu Pro Tyr Gln Asp Lys Val Gly Ala Phe Tyr Lys Asp Asn Ala
 1 5 10 15
 aga gcc aat tca acc aag ctg tcc tta gtg aca gaa gga cat ggg ggc 96
 Arg Ala Asn Ser Thr Lys Leu Ser Leu Val Thr Glu Gly His Gly Gly

	20		25		30	
agg aga cca cct tat ttg ttg ttt gtc ctt ctc atc tta ttg gtt ggt						144
Arg Arg Pro Pro Tyr Leu Leu Phe Val Leu Leu Ile Leu Leu Val Gly						
	35		40		45	
atc ctg gcc ttg ctt gct atc act gga gtt cga ttt cac caa gta tca						192
Ile Leu Ala Leu Leu Ala Ile Thr Gly Val Arg Phe His Gln Val Ser						
	50		55		60	
act agt aat atg gaa ttt agc aga ttg ctg aaa gag gat atg gag aaa						240
Thr Ser Asn Met Glu Phe Ser Arg Leu Leu Lys Glu Asp Met Glu Lys						
	65		70		75	80
tca gag gcc gta cat cac caa gtc ata gat gtc ttg aca ccg ctc ttc						288
Ser Glu Ala Val His His Gln Val Ile Asp Val Leu Thr Pro Leu Phe						
		85		90		95
aag att att gga gat gag att ggg tta cgg ttg cca caa aag cta aac						336
Lys Ile Ile Gly Asp Glu Ile Gly Leu Arg Leu Pro Gln Lys Leu Asn						
	100		105		110	
gag atc aaa caa ttt atc ctt caa aag aca aat ttc ttc aat ccg aac						384
Glu Ile Lys Gln Phe Ile Leu Gln Lys Thr Asn Phe Phe Asn Pro Asn						
	115		120		125	
aga gaa ttc gac ttc cgc gat ctc cac tgg tgc att aac ccg cct agt						432
Arg Glu Phe Asp Phe Arg Asp Leu His Trp Cys Ile Asn Pro Pro Ser						
	130		135		140	
acg gtc aag gtg aat ttt act aat tac tgt gag tca att ggg atc aga						480
Thr Val Lys Val Asn Phe Thr Asn Tyr Cys Glu Ser Ile Gly Ile Arg						
	145		150		155	160
aaa gct att gca tcg gca gca aat cct atc ctt tta tca gcc cta tct						528
Lys Ala Ile Ala Ser Ala Ala Asn Pro Ile Leu Leu Ser Ala Leu Ser						
		165		170		175
ggg ggc aga ggt gac ata ttc cca cca cac aga tgc agt gga gct act						576
Gly Gly Arg Gly Asp Ile Phe Pro Pro His Arg Cys Ser Gly Ala Thr						
	180		185		190	
act tca gta ggc aaa gtt ttc ccc cta tca gtc tca tta tcc atg tct						624
Thr Ser Val Gly Lys Val Phe Pro Leu Ser Val Ser Leu Ser Met Ser						
	195		200		205	
ttg atc tca aga acc tca gag gta atc aat atg ctg acc gct atc tca						672
Leu Ile Ser Arg Thr Ser Glu Val Ile Asn Met Leu Thr Ala Ile Ser						
	210		215		220	
gac ggc gtg tat ggc aaa act tac ttg cta gtg cct gat gat ata gaa						720
Asp Gly Val Tyr Gly Lys Thr Tyr Leu Leu Val Pro Asp Asp Ile Glu						
	225		230		235	240
aga gag ttc gac act cga gag att cga gtc ttt gaa ata ggg ttc atc						768
Arg Glu Phe Asp Thr Arg Glu Ile Arg Val Phe Glu Ile Gly Phe Ile						
		245		250		255

aaa agg tgg ctg aat gac atg cca tta ctc caa aca acc aac tat atg	816
Lys Arg Trp Leu Asn Asp Met Pro Leu Leu Gln Thr Thr Asn Tyr Met	
260 265 270	
gta ctc ccg aag aat tcc aaa gcc aag gta tgt act ata gca gtg ggt	864
Val Leu Pro Lys Asn Ser Lys Ala Lys Val Cys Thr Ile Ala Val Gly	
275 280 285	
gag ttg aca ctg gct tcc ttg tgt gta gaa gag agc act gta tta tta	912
Glu Leu Thr Leu Ala Ser Leu Cys Val Glu Glu Ser Thr Val Leu Leu	
290 295 300	
tat cat gac agc agt ggt tca caa gat ggt att cta gta gtg aca ctg	960
Tyr His Asp Ser Ser Gly Ser Gln Asp Gly Ile Leu Val Val Thr Leu	
305 310 315 320	
ggg ata ttt tgg gca aca cct atg gat cac att gag gaa gtg ata cct	1008
Gly Ile Phe Trp Ala Thr Pro Met Asp His Ile Glu Glu Val Ile Pro	
325 330 335	
gtc gct cac cca tca atg aag aaa ata cat ata aca aac cac cgt ggt	1056
Val Ala His Pro Ser Met Lys Lys Ile His Ile Thr Asn His Arg Gly	
340 345 350	
ttt ata aaa gat tca att gca acc tgg atg gtg cct gcc ctg gcc tct	1104
Phe Ile Lys Asp Ser Ile Ala Thr Trp Met Val Pro Ala Leu Ala Ser	
355 360 365	
gag aaa caa gaa gaa caa aaa ggt tgt ctg gag tca gct tgt caa aga	1152
Glu Lys Gln Glu Glu Gln Lys Gly Cys Leu Glu Ser Ala Cys Gln Arg	
370 375 380	
aaa acc tac ccc atg tgc aac caa gcg tca tgg gaa ccc ttc gga gga	1200
Lys Thr Tyr Pro Met Cys Asn Gln Ala Ser Trp Glu Pro Phe Gly Gly	
385 390 395 400	
aga cag ttg cca tct tat ggg cgg ttg aca tta cct cta gat gca agt	1248
Arg Gln Leu Pro Ser Tyr Gly Arg Leu Thr Leu Pro Leu Asp Ala Ser	
405 410 415	
gtt gac ctt caa ctt aac ata tcg ttc aca tac ggt ccg gtt ata ctg	1296
Val Asp Leu Gln Leu Asn Ile Ser Phe Thr Tyr Gly Pro Val Ile Leu	
420 425 430	
aat gga gat ggt atg gat tat tat gaa agc cca ctt ttg aac tcc gga	1344
Asn Gly Asp Gly Met Asp Tyr Tyr Glu Ser Pro Leu Leu Asn Ser Gly	
435 440 445	
tgg ctt acc att ccc ccc aaa gac gga aca atc tct gga ttg ata aac	1392
Trp Leu Thr Ile Pro Pro Lys Asp Gly Thr Ile Ser Gly Leu Ile Asn	
450 455 460	
aaa gca ggt aga gga gac cag ttc act gta ctc ccc cat gtg tta aca	1440
Lys Ala Gly Arg Gly Asp Gln Phe Thr Val Leu Pro His Val Leu Thr	
465 470 475 480	

ttt gcg ccc agg gaa tca agt gga aat tgt tat tta cct att caa aca	1488
Phe Ala Pro Arg Glu Ser Ser Gly Asn Cys Tyr Leu Pro Ile Gln Thr	
485 490 495	
tct caa att aga gat aga gat gtc ctc att gag tcc aat ata gtg gtg	1536
Ser Gln Ile Arg Asp Arg Asp Val Leu Ile Glu Ser Asn Ile Val Val	
500 505 510	
ttg cct aca cag agt att aga tat gtc ata gca acg tat gac ata tca	1584
Leu Pro Thr Gln Ser Ile Arg Tyr Val Ile Ala Thr Tyr Asp Ile Ser	
515 520 525	
cga agt gat cat gct att gtt tat tat gtt tat gac cca atc cgg acg	1632
Arg Ser Asp His Ala Ile Val Tyr Tyr Val Tyr Asp Pro Ile Arg Thr	
530 535 540	
att tct tat acg cac cca ttt aga cta act acc aag ggt aga cct gat	1680
Ile Ser Tyr Thr His Pro Phe Arg Leu Thr Thr Lys Gly Arg Pro Asp	
545 550 555 560	
ttc cta agg att gaa tgt ttt gtg tgg gat gac aat ttg tgg tgt cac	1728
Phe Leu Arg Ile Glu Cys Phe Val Trp Asp Asp Asn Leu Trp Cys His	
565 570 575	
caa ttt tac aga ttc gag gct gac atc gcc aac tct aca acc agt gtt	1776
Gln Phe Tyr Arg Phe Glu Ala Asp Ile Ala Asn Ser Thr Thr Ser Val	
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Arg Ala Asn Ser Thr Lys Leu Ser Leu Val Thr Glu Gly His Gly Gly	
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35 40 45	
Ile Leu Ala Leu Leu Ala Ile Thr Gly Val Arg Phe His Gln Val Ser	
50 55 60	
Thr Ser Asn Met Glu Phe Ser Arg Leu Leu Lys Glu Asp Met Glu Lys	
65 70 75 80	
Ser Glu Ala Val His His Gln Val Ile Asp Val Leu Thr Pro Leu Phe	
85 90 95	

Lys Ile Ile Gly Asp Glu Ile Gly Leu Arg Leu Pro Gln Lys Leu Asn
 100 105 110
 Glu Ile Lys Gln Phe Ile Leu Gln Lys Thr Asn Phe Phe Asn Pro Asn
 115 120 125
 Arg Glu Phe Asp Phe Arg Asp Leu His Trp Cys Ile Asn Pro Pro Ser
 130 135 140
 Thr Val Lys Val Asn Phe Thr Asn Tyr Cys Glu Ser Ile Gly Ile Arg
 145 150 155 160
 Lys Ala Ile Ala Ser Ala Ala Asn Pro Ile Leu Leu Ser Ala Leu Ser
 165 170 175
 Gly Gly Arg Gly Asp Ile Phe Pro Pro His Arg Cys Ser Gly Ala Thr
 180 185 190
 Thr Ser Val Gly Lys Val Phe Pro Leu Ser Val Ser Leu Ser Met Ser
 195 200 205
 Leu Ile Ser Arg Thr Ser Glu Val Ile Asn Met Leu Thr Ala Ile Ser
 210 215 220
 Asp Gly Val Tyr Gly Lys Thr Tyr Leu Leu Val Pro Asp Asp Ile Glu
 225 230 235 240
 Arg Glu Phe Asp Thr Arg Glu Ile Arg Val Phe Glu Ile Gly Phe Ile
 245 250 255
 Lys Arg Trp Leu Asn Asp Met Pro Leu Leu Gln Thr Thr Asn Tyr Met
 260 265 270
 Val Leu Pro Lys Asn Ser Lys Ala Lys Val Cys Thr Ile Ala Val Gly
 275 280 285
 Glu Leu Thr Leu Ala Ser Leu Cys Val Glu Glu Ser Thr Val Leu Leu
 290 295 300
 Tyr His Asp Ser Ser Gly Ser Gln Asp Gly Ile Leu Val Val Thr Leu
 305 310 315 320
 Gly Ile Phe Trp Ala Thr Pro Met Asp His Ile Glu Glu Val Ile Pro
 325 330 335
 Val Ala His Pro Ser Met Lys Lys Ile His Ile Thr Asn His Arg Gly
 340 345 350
 Phe Ile Lys Asp Ser Ile Ala Thr Trp Met Val Pro Ala Leu Ala Ser
 355 360 365
 Glu Lys Gln Glu Glu Gln Lys Gly Cys Leu Glu Ser Ala Cys Gln Arg
 370 375 380
 Lys Thr Tyr Pro Met Cys Asn Gln Ala Ser Trp Glu Pro Phe Gly Gly
 385 390 395 400

Arg Gln Leu Pro Ser Tyr Gly Arg Leu Thr Leu Pro Leu Asp Ala Ser
 405 410 415
 Val Asp Leu Gln Leu Asn Ile Ser Phe Thr Tyr Gly Pro Val Ile Leu
 420 425 430
 Asn Gly Asp Gly Met Asp Tyr Tyr Glu Ser Pro Leu Leu Asn Ser Gly
 435 440 445
 Trp Leu Thr Ile Pro Pro Lys Asp Gly Thr Ile Ser Gly Leu Ile Asn
 450 455 460
 Lys Ala Gly Arg Gly Asp Gln Phe Thr Val Leu Pro His Val Leu Thr
 465 470 475 480
 Phe Ala Pro Arg Glu Ser Ser Gly Asn Cys Tyr Leu Pro Ile Gln Thr
 485 490 495
 Ser Gln Ile Arg Asp Arg Asp Val Leu Ile Glu Ser Asn Ile Val Val
 500 505 510
 Leu Pro Thr Gln Ser Ile Arg Tyr Val Ile Ala Thr Tyr Asp Ile Ser
 515 520 525
 Arg Ser Asp His Ala Ile Val Tyr Tyr Val Tyr Asp Pro Ile Arg Thr
 530 535 540
 Ile Ser Tyr Thr His Pro Phe Arg Leu Thr Thr Lys Gly Arg Pro Asp
 545 550 555 560
 Phe Leu Arg Ile Glu Cys Phe Val Trp Asp Asp Asn Leu Trp Cys His
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 580 585 590
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<210> 35
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<220>
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<400> 35
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 1 5 10 15
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 Gln Asp Arg Pro Pro Gln Pro Ser Thr Glu Leu Glu Glu Thr Arg Thr

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tcc	cga	gca	cga	cac	agc	aca	aca	tca	gct	cag	cga	tcc	acg	cac	tac	144
Ser	Arg	Ala	Arg	His	Ser	Thr	Thr	Ser	Ala	Gln	Arg	Ser	Thr	His	Tyr	
		35					40					45				
gat	cct	cga	aca	tcg	gac	aga	ccc	gtc	tcc	tac	acc	atg	aac	agg	acc	192
Asp	Pro	Arg	Thr	Ser	Asp	Arg	Pro	Val	Ser	Tyr	Thr	Met	Asn	Arg	Thr	
	50					55					60					
agg	tcc	cgc	aag	caa	acc	agc	cac	aga	ttg	aag	aac	atc	cca	gtt	cac	240
Arg	Ser	Arg	Lys	Gln	Thr	Ser	His	Arg	Leu	Lys	Asn	Ile	Pro	Val	His	
	65				70					75					80	
gga	aac	cac	gag	gcc	acc	atc	cag	cac	ata	cca	gag	agt	gtc	tca	aaa	288
Gly	Asn	His	Glu	Ala	Thr	Ile	Gln	His	Ile	Pro	Glu	Ser	Val	Ser	Lys	
			85					90						95		
gga	gcg	aga	tcc	cag	atc	gaa	agg	cgg	caa	ccc	aat	gca	atc	aac	tca	336
Gly	Ala	Arg	Ser	Gln	Ile	Glu	Arg	Arg	Gln	Pro	Asn	Ala	Ile	Asn	Ser	
			100					105						110		
ggc	tct	cat	tgc	acc	tgg	tta	gtc	ctg	tgg	tgc	ctc	gga	atg	gcc	agt	384
Gly	Ser	His	Cys	Thr	Trp	Leu	Val	Leu	Trp	Cys	Leu	Gly	Met	Ala	Ser	
		115					120						125			
ctc	ttt	ctt	tgt	tcc	aag	gct	cag	ata	cat	tgg	gat	aat	ttg	tca	act	432
Leu	Phe	Leu	Cys	Ser	Lys	Ala	Gln	Ile	His	Trp	Asp	Asn	Leu	Ser	Thr	
	130					135					140					
att	ggg	att	atc	ggg	act	gat	aat	gtc	cat	tac	aag	atc	atg	act	agg	480
Ile	Gly	Ile	Ile	Gly	Thr	Asp	Asn	Val	His	Tyr	Lys	Ile	Met	Thr	Arg	
	145				150					155					160	
ccc	agt	cac	cag	tac	ttg	gtc	ata	aaa	ttg	atc	cct	aat	gct	tca	ctt	528
Pro	Ser	His	Gln	Tyr	Leu	Val	Ile	Lys	Leu	Ile	Pro	Asn	Ala	Ser	Leu	
			165					170						175		
ata	gag	aat	tgt	acc	aaa	gca	gaa	tta	ggg	gag	tat	gag	aaa	tta	ttg	576
Ile	Glu	Asn	Cys	Thr	Lys	Ala	Glu	Leu	Gly	Glu	Tyr	Glu	Lys	Leu	Leu	
			180					185						190		
aat	tca	gtc	ctc	gaa	cca	atc	aac	caa	gct	ttg	act	cta	atg	acc	aag	624
Asn	Ser	Val	Leu	Glu	Pro	Ile	Asn	Gln	Ala	Leu	Thr	Leu	Met	Thr	Lys	
		195					200					205				
aat	gtg	aag	ccc	ctg	cag	tca	tta	ggg	tca	ggg	agg	aga	caa	agg	cgt	672
Asn	Val	Lys	Pro	Leu	Gln	Ser	Leu	Gly	Ser	Gly	Arg	Arg	Gln	Arg	Arg	
	210					215					220					
ttt	gca	gga	gtg	gta	ctt	gca	ggg	gta	gct	tta	gga	gtg	gct	aca	gct	720
Phe	Ala	Gly	Val	Val	Leu	Ala	Gly	Val	Ala	Leu	Gly	Val	Ala	Thr	Ala	
	225				230					235					240	
gca	caa	atc	act	gca	gga	ata	gct	tta	cat	caa	tcc	aac	ctc	aat	gct	768
Ala	Gln	Ile	Thr	Ala	Gly	Ile	Ala	Leu	His	Gln	Ser	Asn	Leu	Asn	Ala	
				245					250						255	

caa gca atc caa tct ctt aga acc agc ctt gaa cag tct aac aaa gct	816
Gln Ala Ile Gln Ser Leu Arg Thr Ser Leu Glu Gln Ser Asn Lys Ala	
260 265 270	
ata gaa gaa att agg gag gct acc caa gaa acc gtc att gcc gtt cag	864
Ile Glu Glu Ile Arg Glu Ala Thr Gln Glu Thr Val Ile Ala Val Gln	
275 280 285	
gga gtc cag gac tac gtc aac aac gaa ctc gtc cct gcc atg caa cat	912
Gly Val Gln Asp Tyr Val Asn Asn Glu Leu Val Pro Ala Met Gln His	
290 295 300	
atg tca tgt gaa tta gtt ggg cag aga tta ggg tta aga ctg ctt cgg	960
Met Ser Cys Glu Leu Val Gly Gln Arg Leu Gly Leu Arg Leu Leu Arg	
305 310 315 320	
tat tat act gag ttg ttg tca ata ttt ggc ccg agt tta cgt gac cct	1008
Tyr Tyr Thr Glu Leu Leu Ser Ile Phe Gly Pro Ser Leu Arg Asp Pro	
325 330 335	
att tca gcc gag ata tca att cag gca ctg att tat gct ctt gga gga	1056
Ile Ser Ala Glu Ile Ser Ile Gln Ala Leu Ile Tyr Ala Leu Gly Gly	
340 345 350	
gaa att cat aag ata ctt gag aag ttg gga tat tct gga agt gat atg	1104
Glu Ile His Lys Ile Leu Glu Lys Leu Gly Tyr Ser Gly Ser Asp Met	
355 360 365	
att gca atc ttg gag agt cgg ggg ata aaa aca aaa ata act cat gtt	1152
Ile Ala Ile Leu Glu Ser Arg Gly Ile Lys Thr Lys Ile Thr His Val	
370 375 380	
gat ctt ccc ggg aaa ttc atc atc cta agt atc tca tac cca act tta	1200
Asp Leu Pro Gly Lys Phe Ile Ile Leu Ser Ile Ser Tyr Pro Thr Leu	
385 390 395 400	
tca gaa gtc aag ggg gtt ata gtc cac aga ctg gaa gca gtt tct tac	1248
Ser Glu Val Lys Gly Val Ile Val His Arg Leu Glu Ala Val Ser Tyr	
405 410 415	
aac ata gga tca caa gag tgg tac acc act gtc ccg agg tat att gca	1296
Asn Ile Gly Ser Gln Glu Trp Tyr Thr Thr Val Pro Arg Tyr Ile Ala	
420 425 430	
act aat ggt tac tta ata tct aat ttt gat gag tca tct tgt gta ttc	1344
Thr Asn Gly Tyr Leu Ile Ser Asn Phe Asp Glu Ser Ser Cys Val Phe	
435 440 445	
gtc tca gag tca gcc att tgt agc cag aac tcc ctg tat ccc atg agc	1392
Val Ser Glu Ser Ala Ile Cys Ser Gln Asn Ser Leu Tyr Pro Met Ser	
450 455 460	
cca ctc tta caa caa tgt att agg ggc gac act tca tct tgt gct cgg	1440
Pro Leu Leu Gln Gln Cys Ile Arg Gly Asp Thr Ser Ser Cys Ala Arg	
465 470 475 480	

acc ttg gta tct ggg act atg ggc aac aaa ttt att ctg tca aaa ggt	1488
Thr Leu Val Ser Gly Thr Met Gly Asn Lys Phe Ile Leu Ser Lys Gly	
485 490 495	
aat atc gtc gca aat tgt gct tct ata cta tgt aag tgt tat agc aca	1536
Asn Ile Val Ala Asn Cys Ala Ser Ile Leu Cys Lys Cys Tyr Ser Thr	
500 505 510	
agc aca att att aat cag agt cct gat aag ttg ctg aca ttc att gcc	1584
Ser Thr Ile Ile Asn Gln Ser Pro Asp Lys Leu Leu Thr Phe Ile Ala	
515 520 525	
tcc gat acc tgc cca ctg gtt gaa ata gat ggt gct act atc caa gtt	1632
Ser Asp Thr Cys Pro Leu Val Glu Ile Asp Gly Ala Thr Ile Gln Val	
530 535 540	
gga ggc agg caa tac cct gat atg gta tac gaa ggc aaa gtt gcc tta	1680
Gly Gly Arg Gln Tyr Pro Asp Met Val Tyr Glu Gly Lys Val Ala Leu	
545 550 555 560	
ggc cct gct ata tca ctt gat agg tta gat gta ggt aca aac tta ggg	1728
Gly Pro Ala Ile Ser Leu Asp Arg Leu Asp Val Gly Thr Asn Leu Gly	
565 570 575	
aac gcc ctt aag aaa ctg gat gat gct aag gta ctg ata gac tcc tct	1776
Asn Ala Leu Lys Lys Leu Asp Asp Ala Lys Val Leu Ile Asp Ser Ser	
580 585 590	
aac cag atc ctt gag acg gtt agg cgc tct tcc ttt aat ttt ggc agt	1824
Asn Gln Ile Leu Glu Thr Val Arg Arg Ser Ser Phe Asn Phe Gly Ser	
595 600 605	
ctc ctc agc gtt cct ata tta agt tgt aca gcc ctg gct ttg ttg ttg	1872
Leu Leu Ser Val Pro Ile Leu Ser Cys Thr Ala Leu Ala Leu Leu Leu	
610 615 620	
ctg att tac tgt tgt aaa aga cgc tac caa cag aca ctc aag cag cat	1920
Leu Ile Tyr Cys Cys Lys Arg Arg Tyr Gln Gln Thr Leu Lys Gln His	
625 630 635 640	
act aag gtc gat ccg gca ttt aaa cct gat cta act gga act tcg aaa	1968
Thr Lys Val Asp Pro Ala Phe Lys Pro Asp Leu Thr Gly Thr Ser Lys	
645 650 655	
tcc tat gtg aga tca ctc	1986
Ser Tyr Val Arg Ser Leu	
660	

<210> 36

<211> 662

<212> PRT

<213> canine distemper virus

<400> 36

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 Ser Arg Ala Arg His Ser Thr Thr Ser Ala Gln Arg Ser Thr His Tyr
 35 40 45
 Asp Pro Arg Thr Ser Asp Arg Pro Val Ser Tyr Thr Met Asn Arg Thr
 50 55 60
 Arg Ser Arg Lys Gln Thr Ser His Arg Leu Lys Asn Ile Pro Val His
 65 70 75 80
 Gly Asn His Glu Ala Thr Ile Gln His Ile Pro Glu Ser Val Ser Lys
 85 90 95
 Gly Ala Arg Ser Gln Ile Glu Arg Arg Gln Pro Asn Ala Ile Asn Ser
 100 105 110
 Gly Ser His Cys Thr Trp Leu Val Leu Trp Cys Leu Gly Met Ala Ser
 115 120 125
 Leu Phe Leu Cys Ser Lys Ala Gln Ile His Trp Asp Asn Leu Ser Thr
 130 135 140
 Ile Gly Ile Ile Gly Thr Asp Asn Val His Tyr Lys Ile Met Thr Arg
 145 150 155 160
 Pro Ser His Gln Tyr Leu Val Ile Lys Leu Ile Pro Asn Ala Ser Leu
 165 170 175
 Ile Glu Asn Cys Thr Lys Ala Glu Leu Gly Glu Tyr Glu Lys Leu Leu
 180 185 190
 Asn Ser Val Leu Glu Pro Ile Asn Gln Ala Leu Thr Leu Met Thr Lys
 195 200 205
 Asn Val Lys Pro Leu Gln Ser Leu Gly Ser Gly Arg Arg Gln Arg Arg
 210 215 220
 Phe Ala Gly Val Val Leu Ala Gly Val Ala Leu Gly Val Ala Thr Ala
 225 230 235 240
 Ala Gln Ile Thr Ala Gly Ile Ala Leu His Gln Ser Asn Leu Asn Ala
 245 250 255
 Gln Ala Ile Gln Ser Leu Arg Thr Ser Leu Glu Gln Ser Asn Lys Ala
 260 265 270
 Ile Glu Glu Ile Arg Glu Ala Thr Gln Glu Thr Val Ile Ala Val Gln
 275 280 285
 Gly Val Gln Asp Tyr Val Asn Asn Glu Leu Val Pro Ala Met Gln His
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 Met Ser Cys Glu Leu Val Gly Gln Arg Leu Gly Leu Arg Leu Leu Arg
 305 310 315 320

Tyr Tyr Thr Glu Leu Leu Ser Ile Phe Gly Pro Ser Leu Arg Asp Pro
325 330 335
Ile Ser Ala Glu Ile Ser Ile Gln Ala Leu Ile Tyr Ala Leu Gly Gly
340 345 350
Glu Ile His Lys Ile Leu Glu Lys Leu Gly Tyr Ser Gly Ser Asp Met
355 360 365
Ile Ala Ile Leu Glu Ser Arg Gly Ile Lys Thr Lys Ile Thr His Val
370 375 380
Asp Leu Pro Gly Lys Phe Ile Ile Leu Ser Ile Ser Tyr Pro Thr Leu
385 390 395 400
Ser Glu Val Lys Gly Val Ile Val His Arg Leu Glu Ala Val Ser Tyr
405 410 415
Asn Ile Gly Ser Gln Glu Trp Tyr Thr Thr Val Pro Arg Tyr Ile Ala
420 425 430
Thr Asn Gly Tyr Leu Ile Ser Asn Phe Asp Glu Ser Ser Cys Val Phe
435 440 445
Val Ser Glu Ser Ala Ile Cys Ser Gln Asn Ser Leu Tyr Pro Met Ser
450 455 460
Pro Leu Leu Gln Gln Cys Ile Arg Gly Asp Thr Ser Ser Cys Ala Arg
465 470 475 480
Thr Leu Val Ser Gly Thr Met Gly Asn Lys Phe Ile Leu Ser Lys Gly
485 490 495
Asn Ile Val Ala Asn Cys Ala Ser Ile Leu Cys Lys Cys Tyr Ser Thr
500 505 510
Ser Thr Ile Ile Asn Gln Ser Pro Asp Lys Leu Leu Thr Phe Ile Ala
515 520 525
Ser Asp Thr Cys Pro Leu Val Glu Ile Asp Gly Ala Thr Ile Gln Val
530 535 540
Gly Gly Arg Gln Tyr Pro Asp Met Val Tyr Glu Gly Lys Val Ala Leu
545 550 555 560
Gly Pro Ala Ile Ser Leu Asp Arg Leu Asp Val Gly Thr Asn Leu Gly
565 570 575
Asn Ala Leu Lys Lys Leu Asp Asp Ala Lys Val Leu Ile Asp Ser Ser
580 585 590
Asn Gln Ile Leu Glu Thr Val Arg Arg Ser Ser Phe Asn Phe Gly Ser
595 600 605
Leu Leu Ser Val Pro Ile Leu Ser Cys Thr Ala Leu Ala Leu Leu Leu
610 615 620

Leu	Ile	Tyr	Cys	Cys	Lys	Arg	Arg	Tyr	Gln	Gln	Thr	Leu	Lys	Gln	His
625					630					635					640
Thr	Lys	Val	Asp	Pro	Ala	Phe	Lys	Pro	Asp	Leu	Thr	Gly	Thr	Ser	Lys
				645					650					655	
Ser	Tyr	Val	Arg	Ser	Leu										
				660											